

FIGURE 1

	gcggccgccc	ctgacacaat	ggctcagctt	atgcctcagc	gcagttcgc	ccaccccaga		60
5	atggcaccct	gcagaataca	cggccccctca	tccccatccc	gcgccagaga	caccggccag		120
	cccactgtcc	ccgccacaca	ttaaacttga	tcctcctaca	cagacgcact	cggagcagag		180
	cgcttatata	agcgcacagc	cgtctccggc	accgccacac	agacagatga	tgccgccccg		240
	accgacggcc	agccccagac	acaaccttct	gaaaacacag	aaaacaagtc	ccagcccaag		300
	cggctgcatg	tgtccaacat	ccccttccgg	ttccgggata	cagacctccg	acaaatgttt		360
10	ggccaatttg	gtaaaatatt	agatgttgaa	attattttta	atgagcgggg	ctcgaaggga		420
	tttggtttcg	taactttcga	aaatagtgcg	gatgcggaca	gggcgaggga	gaaattgcac		480
	ggtaccgtgg	tagagggccg	taaaatcgag	gttaataatg	cgacagcacg	cgtg atg		537
						Met		
						1		
15								
	act aat aaa aag gcc gtg aac ccc tac acc aat ggc tgg aaa tta aat							585
	Thr Asn Lys Lys Ala Val Asn Pro Tyr Thr Asn Gly Trp Lys Leu Asn							
		5					15	
20								
	cca gtt gtg ggc gcg gtc tac agc ccc gac ttc tat gca ggc acg gtg							633
	Pro Val Val Gly Ala Val Tyr Ser Pro Asp Phe Tyr Ala Gly Thr Val							
		20					30	
25								
	ctg ttg tgc cag gcc aac cag gag gga tct tcc atg tac agt ggc ccc							681
	Leu Leu Cys Gln Ala Asn Gln Glu Gly Ser Ser Met Tyr Ser Gly Pro							
		35					45	
30								
	agt tca ctt gta tat act tct gca atg cct ggc ttt cca tat ccg gcc							729
	Ser Ser Leu Val Tyr Thr Ser Ala Met Pro Gly Phe Pro Tyr Pro Ala							
		50					60	65
35								
	gcc act gct gca gct gca tac cga ggg gct cac ctt cga ggc cgt ggt							777
	Ala Thr Ala Ala Ala Tyr Arg Gly Ala His Leu Arg Gly Arg Gly							
			70				75	80
40								
	cgc acc gtg tac aac acc ttc aga gct gcg gcg ccc cca ccc cca atc							825
	Arg Thr Val Tyr Asn Thr Phe Arg Ala Ala Ala Pro Pro Pro Pro Ile							
			85				90	95
45								
	ccg gcc tat ggc gga gta gtg tat caa gag cca gtg tat ggc aat aaa							873
	Pro Ala Tyr Gly Gly Val Val Tyr Gln Glu Pro Val Tyr Gly Asn Lys							
		100					105	110
50								
	ttg cta cag ggt ggt tac gct gca tac cgc tac gcc cag ccc acc cct							921
	Leu Leu Gln Gly Gly Tyr Ala Ala Tyr Arg Tyr Ala Gln Pro Thr Pro							
		115					120	125
55								
	gcc act gct gct gcc tac agt gac agt tac gga cga gtt tat gct gcc							969
	Ala Thr Ala Ala Ala Tyr Ser Asp Ser Tyr Gly Arg Val Tyr Ala Ala							
		130					135	140
60								
	gac ccc tac cac cac aca ctt gct cca gcc ccc acc tac ggc gtt ggt							1017
	Asp Pro Tyr His His Thr Leu Ala Pro Ala Pro Thr Tyr Gly Val Gly							
			150				155	160
65								
	gcc atg aat gct ttt gcg ccc ttg acc gat gcc aag act aag agc cat							1065

FIGURE 1 (cont.)

5	Ala Met Asn Ala Phe Ala Pro Leu Thr Asp Ala Lys Thr Arg Ser His	
	165 170 175	
	gct gat gat gtg ggt ctc gtt ctt tct tca ttg cag gct agt ata tac	1113
10	Ala Asp Asp Val Gly Leu Val Leu Ser Ser Leu Gln Ala Ser Ile Tyr	
	180 185 190	
	caa ggg gga tac aac cgt ttt gct cca tat taaatgataa aaccattaaa	1163
	Gln Gly Gly Tyr Asn Arg Phe Ala Pro Tyr	
	195 200	
15	caaacaagca aaaaacaaaa caaaaacaaa aaaaccaacc ttccaatgtg gggagagagg	1223
	aagctttccg aggcccgagt gttgcgacac atgcagtagg acatcacttt agcaactcaa	1283
	agaaacaacg aaaaaaaaaa aaaaaaaaaa aataagcggc cgaagggggt cgctaga	1340
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FIGURE 2

5	tctagcgaac cccttcgcga aggggttcgc ctgtgctggg gggcgcggtg gcccgaagcc	60
	ttggactcac tgcaggactg tgcagggaac cactgtccaa gcatcgggct aatagggggc	120
	gcctgcctcg gtttaccctt cagcgtctgg tgaaatcccg cagcgtctag ggaaagatcc	180
	gttctgctcc gcgagggaaa cagagccgtt gacc atg gtt gca acg ggc agt ttg	235
	Met Val Ala Thr Gly Ser Leu	
10	1 5	
	agc agt aag aac acg gcc agc att tca gag ttg ctg gac ggt ggc tct	283
	Ser Ser Lys Asn Thr Ala Ser Ile Ser Glu Leu Leu Asp Gly Gly Ser	
	10 15 20	
15	cac cct ggg agt ctg cta agt gat ttc gac tac tgg gat tat gtc gtc	331
	His Pro Gly Ser Leu Leu Ser Asp Phe Asp Tyr Trp Asp Tyr Val Val	
	25 30 35	
20	cct gag ccc aac ctc aac gag gtg gtg ttt gaa gag aca aca tgc cag	379
	Pro Glu Pro Asn Leu Asn Glu Val Val Phe Glu Glu Thr Thr Cys Gln	
	40 45 50 55	
25	aat ttg gtt aaa atg ttg gag aac tgt ctg tcc aag tca aag caa acc	427
	Asn Leu Val Lys Met Leu Glu Asn Cys Leu Ser Lys Ser Lys Gln Thr	
	60 65 70	
30	aaa ctc ggt tgc tct aag gtc ctg gtt cct gag aaa ctg acc cag aga	475
	Lys Leu Gly Cys Ser Lys Val Leu Val Pro Glu Lys Leu Thr Gln Arg	
	75 80 85	
35	att gcc caa gat gtc ctg cgg ctc tca tcc aca gag ccc tgc ggc ctt	523
	Ile Ala Gln Asp Val Leu Arg Leu Ser Ser Thr Glu Pro Cys Gly Leu	
	90 95 100	
40	cgg ggc tgt gtt atg cac gtg aac ttg gaa att gaa aat gtg tgt aaa	571
	Arg Gly Cys Val Met His Val Asn Leu Glu Ile Glu Asn Val Cys Lys	
	105 110 115	
45	aag ctg gat agg att gtg tgt gat gct agt gtg gtg ccg acc ttt gag	619
	Lys Leu Asp Arg Ile Val Cys Asp Ala Ser Val Val Pro Thr Phe Glu	
	120 125 130 135	
50	ctc acg ctg gtg ttc aag cag gag agc tgc tcc tgg acc agc ctc aag	667
	Leu Thr Leu Val Phe Lys Gln Glu Ser Cys Ser Trp Thr Ser Leu Lys	
	140 145 150	
55	gac ttc ttc ttt agc gga ggt cgc ttc tcg tcg ggc ctt aag cga act	715
	Asp Phe Phe Phe Ser Gly Gly Arg Phe Ser Ser Gly Leu Lys Arg Thr	
	155 160 165	
60	ctg atc ctc agc tcg gga ttt cga ctt gtt aag aaa aaa ctg tac tct	763
	Leu Ile Leu Ser Ser Gly Phe Arg Leu Val Lys Lys Lys Leu Tyr Ser	
	170 175 180	
65	ctg att gga acg aca gtc att gag gag tgc tga ggaggaaaaa acaattaaag	816
	Leu Ile Gly Thr Thr Val Ile Glu Glu Cys *	

FIGURE 2 (cont.)

5 gtcctaag agtggctaac aaaaanaaaa nnnnnnnnnn nnnnngcggn c

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185 190
gtcctaag agtggctaac aaaaanaaaa nnnnnnnnnn nnnnngcggn c
867

FIGURE 3

5	tctagcgaac cccttcgggtg gacagaacag cctgagtcag g atg aaa gct ctc agg	56
	Met Lys Ala Leu Arg	
	1 5	
10	gct gtc ctc ctg atc ttg cta ctc agt gga cag cca ggg agc agc tgg	104
	Ala Val Leu Leu Ile Leu Leu Leu Ser Gly Gln Pro Gly Ser Ser Trp	
	10 15 20	
15	gca caa gaa gct ggc gat gtg gac ctg gag cta gag cgc tac agc tac	152
	Ala Gln Glu Ala Gly Asp Val Asp Leu Glu Leu Glu Arg Tyr Ser Tyr	
	25 30 35	
20	gat gat gac ggt gat gac gat gat gac gat gat gaa gaa gag gaa gag	200
	Asp Asp Asp Gly Asp Asp Asp Asp Asp Asp Asp Glu Glu Glu Glu Glu	
	40 45 50	
25	gag gag acc aac atg atc cct ggc agc agg gac aga gca ccg cct cta	248
	Glu Glu Thr Asn Met Ile Pro Gly Ser Arg Asp Arg Ala Pro Pro Leu	
	55 60 65	
30	cag tgc tac ttc tgc caa gtg ctt cac agc ggg gag agc tgc aac gag	296
	Gln Cys Tyr Phe Cys Gln Val Leu His Ser Gly Glu Ser Cys Asn Glu	
	70 75 80 85	
35	aca cag aga tgc tcc agc agc aag ccc ttc tgt atc aca gtc atc tcc	344
	Thr Gln Arg Cys Ser Ser Ser Lys Pro Phe Cys Ile Thr Val Ile Ser	
	90 95 100	
40	cat ggc aaa act gac aca ggt gtc ctg acg acc tac tcc atg tgg tgt	392
	His Gly Lys Thr Asp Thr Gly Val Leu Thr Thr Tyr Ser Met Trp Cys	
	105 110 115	
45	act gat acc tgc cag ccc atc gtg aag aca gtg gac agc acc caa atg	440
	Thr Asp Thr Cys Gln Pro Ile Val Lys Thr Val Asp Ser Thr Gln Met	
	120 125 130	
50	acc cag acc tgt tgc cag tcc aca ctc tgc aat att cca ccc tgg cag	488
	Thr Gln Thr Cys Cys Gln Ser Thr Leu Cys Asn Ile Pro Pro Trp Gln	
	135 140 145	
55	agc ccc caa atc cac aac cct ctg ggt ggc cgg gca gac agc ccc ttg	536
	Ser Pro Gln Ile His Asn Pro Leu Gly Gly Arg Ala Asp Ser Pro Leu	
	150 155 160 165	
60	aag ggt ggg acc aga cat cct caa ggt gac agg ttt agc cac ccc cag	584
	Lys Gly Gly Thr Arg His Pro Gln Gly Asp Arg Phe Ser His Pro Gln	
	170 175 180	
65	gtt gtc aag gtt act cat cct cag agt gat ggg gct cac ttg tct aag	632
	Val Val Lys Val Thr His Pro Gln Ser Asp Gly Ala His Leu Ser Lys	
	185 190 195	
70	ggt ggc aag gct aac cag ccc cag gga aat ggg gcc gga ttc cct gca	680

FIGURE 3 (cont.)

5	Gly Gly Lys Ala Asn Gln Pro Gln Gly Asn Gly Ala Gly Phe Pro Ala	
	200 205 210	
	ggc tgg agc aaa ttt ggt aac gta gtt ctc ctg ctc acc ttc ctc acc	728
10	Gly Trp Ser Lys Phe Gly Asn Val Val Leu Leu Leu Thr Phe Leu Thr	
	215 220 225	
	agt ctg tgg gca tca ggg gcc taa agactcgtcc tcccccaacc aggacccttc	782
	Ser Leu Trp Ala Ser Gly Ala *	
	230 235	
15	agccttttct cctgacaac cagcttcaga gaataaaactt gaatgtcttt tgccatctaa	842
	aaaaaaaaa aaaaaaaaaa aaagcggcgcg cc	874
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FIGURE 4

5	tctagcgaac cccttcgagc gaaccccttc ggccagtacc ctgagccctg gtcctctctg	60
	gagctgcccc acagctctga ctgtggactg agggatgtta ggcggatcac ctgagcctcc	120
	agaggctcac acta atg agc ggg cgc tct ctt ctt agc cac tgt tgc att	170
	Met Ser Gly Arg Ser Leu Leu Ser His Cys Cys Ile	
	1 5 10	
10	tgg ttt tca ttg act cct ggg cct cgt ttg agt gac act gtc ctt gtc	218
	Trp Phe Ser Leu Thr Pro Gly Pro Arg Leu Ser Asp Thr Val Leu Val	
	15 20 25	
15	ttt tgt ttc aga gct ctc cca gtg tta gtg gac tca gat gag gaa att	266
	Phe Cys Phe Arg Ala Leu Pro Val Leu Val Asp Ser Asp Glu Glu Ile	
	30 35 40	
20	atg acc aga tct gaa ata gct gaa aaa atg ttc tct tca gaa aag ata	314
	Met Thr Arg Ser Glu Ile Ala Glu Lys Met Phe Ser Ser Glu Lys Ile	
	45 50 55 60	
25	atg tga tcagggcccc agtgggtcca gtgtgcatgg gagcgcggtc agtgatggg	370
	Met *	
30	aaaggcctgg ctctcgtcaa aactgacagc tgcgctatga tacatgtctc actttgttgt	430
	cttgagatc tgtgtatgca ggtgaagaac tcaagtgtgg gagggctctgc cgcctcagaa	490
	agccatcttt gaaacggact cataaagtca gttttgttgc cattaagttg cctgattttg	550
	gaaacaattt aagaagtgtt aaagacatgt gttcagatgc ctcttaggcg gcagccacag	610
	gcatgccagg ttgtgtccct cagttttctc cagacaaaag aatctgcagc tgggcgtggc	670
	ggcacactac tggcagttga aagtctgtaa tttcaaggcc aagcctggtc tacatagttc	730
	caggacaacc agagagatct acatagttag accctgcctc aaaacacaga aaccnnanna	790
	naaaaaaaaa aaaaaaaaaa cgccgc	817
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FIGURE 5

5	tctagcgaac cccttcgcac atgggttcct gctgaccaag gggacatggc tctgaagatg	60
	atgaggctgg ttactcagca ggagtagctg agctgagctg gccctggagg ccctggaggc	120
	cctggagtag ggcccagg atg cag gtg cta atg tct atc ccc ggc gct ctt	171
	Met Gln Val Leu Met Ser Ile Pro Gly Ala Leu	
	1 5 10	
10	ctt ccc gac tct acc atg gga tgt aac tcc agg agc ccc tgc cat ctc	219
	Leu Pro Asp Ser Thr Met Gly Cys Asn Ser Arg Ser Pro Cys His Leu	
	15 20 25	
15	ccg tac caa aag act gtg gct tcc gtg tct act cag aaa tca gtt cta	267
	Pro Tyr Gln Lys Thr Val Ala Ser Val Ser Thr Gln Lys Ser Val Leu	
	30 35 40	
20	ctt cgt aaa cag tgt tta aaa cca gac tca ttt aat cag agt gaa gga	315
	Leu Arg Lys Gln Cys Leu Lys Pro Asp Ser Phe Asn Gln Ser Glu Gly	
	45 50 55	
25	ttg cag tcc att ggc ttc tta gca cag aag cag ctg ata aca caa gta	363
	Leu Gln Ser Ile Gly Phe Leu Ala Gln Lys Gln Leu Ile Thr Gln Val	
	60 65 70 75	
30	aac ccc agc cct tga gaggtagaag caagaggatc agagggttcaa gcgcaccc	418
	Asn Pro Ser Pro *	
35	ggctccatca caagttcaaa agccgcctgc accaaatggg agtccttgct tcaaaaaaaaa	478
	aaaaaaaaaa agcaaagaaa gcaaaggact cgatgacatg atttatagac aaaagcagtg	538
	ggagaaaata ctaaagcccc actgagctgc cagccaggtg tctgtgacta caggtctttt	598
	atctgctcat atatatTTTT acaaaaaatg aaattcatat tggtcgctat tttgctggct	658
	gctttgctcc cgatcaacat gatttgcacg ttttttccat caataaatgt gccatgatat	718
	ttttaaaaaa aaaaaaaaaa aaaaaaaaaa gggcncc	755
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FIGURE 6

5	tctagcgaac cccttgcag ctctctgacc tgcgtgcgcg ccgctctccg ctcttgattt	60
	cgccgtg atg tcg acc gca atg aac ttc ggg acc aaa agc ttc cag ccg	109
	Met Ser Thr Ala Met Asn Phe Gly Thr Lys Ser Phe Gln Pro	
	1 5 10	
10	cgg ccc cca gac aaa ggc agc ttc ccg cta gac cac ttc ggt gag tgt	157
	Arg Pro Pro Asp Lys Gly Ser Phe Pro Leu Asp His Phe Gly Glu Cys	
	15 20 25 30	
15	aaa agc ttt aag gaa aaa ttc atg aag tgt ctc cgc gac aag aac tat	205
	Lys Ser Phe Lys Glu Lys Phe Met Lys Cys Leu Arg Asp Lys Asn Tyr	
	35 40 45	
20	gaa aat gct ctg tgc aga aat gaa tct aaa gag tat tta atg tgc agg	253
	Glu Asn Ala Leu Cys Arg Asn Glu Ser Lys Glu Tyr Leu Met Cys Arg	
	50 55 60	
25	atg caa agg cag ctg atg gca cca gaa cca cta gag aaa ctc ggc ttt	301
	Met Gln Arg Gln Leu Met Ala Pro Glu Pro Leu Glu Lys Leu Gly Phe	
	65 70 75	
30	aga gac ata atg gag gag aaa ccg gag gca aag gac aaa tgt tga	346
	Arg Asp Ile Met Glu Glu Lys Pro Glu Ala Lys Asp Lys Cys *	
	80 85 90	
35	gaatcactgg gctgtgtccc cctacctgga gcagagctga gcccttctgc ccaccgtgga	406
	gagagctgag ccatacctgtg ctgccagag gaggggctct ccgtgtcgac tttggctcat	466
	ccctgcagca cagaccaaac tgctttctct actgaccaca cttctgcttc agagagnggt	526
	ttctcctgtc tngtgtggc acaggatctg ctcanngctg aacactgatg tgatatgata	586
	tcccacctag tgtggccgca caccaaaagg cctggacagg atttcacagt gactcaacct	646
	gagtcctcac acccggaacc tgtcagcgaa aaccaancga agcaaaatgn ctggcttttg	706
	gcttacaaac cccatnattt gntttccctt ctcttgggtc tttgttttga caaanctggc	766
	atacaaagtn ggaaggggga aataaaaaaa aaaaaaaaaa	806
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FIGURE 7

5	tctagcgaac cccttcncga aggggttcgc cgagaggtgg gagccaaaag gatggagcat	60
	ccgccggtgg tggctggtgg ccgcaatctt ggtggtcctg atcggggttg tcttagtctg	120
	cctgatagtc tacttcgcca acgcagcgca cagcgaggcc tgtaagaacg ggttcggtt	180
	gcaggatgag tgccgaaaca ccacgcacct gttgaagcac cagctnaccg gcgcccagga	240
	cagcctgctg cagacggag atg cag gca aac tcc tgc aac cag acc gtg atg	292
10	Met Gln Ala Asn Ser Cys Asn Gln Thr Val Met	
	1 5 10	
	gac ctt cgg gat tcc ctg aag aag aag gtg tct naa acc cag gag caa	340
	Asp Leu Arg Asp Ser Leu Lys Lys Lys Val Ser Xaa Thr Gln Glu Gln	
15	15 20 25	
	can gcc cgc atc aag gaa ctt gag aat aag atc gag agg ctg aac caa	388
	Xaa Ala Arg Ile Lys Glu Leu Glu Asn Lys Ile Glu Arg Leu Asn Gln	
	30 35 40	
20	gag ctg gag aaa ttt gag gac cca aaa gga aat ttc tac cac agt gca	436
	Glu Leu Glu Lys Phe Glu Asp Pro Lys Gly Asn Phe Tyr His Ser Ala	
	45 50 55	
25	ngt gaa ctc aag cgg gtt cgt ggt ggn ctt can cct act tgt gct ttg	484
	Xaa Glu Leu Lys Arg Val Arg Gly Gly Leu Xaa Pro Thr Cys Ala Leu	
	60 65 70 75	
	tgg cgg gac tgt tct nca ctt ttt ang acc caa taa ttgggangta	530
30	Trp Arg Asp Cys Ser Xaa Leu Phe Xaa Thr Gln *	
	80 85	
	caaacctgtg taggcattgn nggtngtaat ggcttttgag ggggtcctgg cacccttaag	590
	atgtgaanac cattangnng gacccaaaat gnnttttctt gntttgaact gggcgacc	650
35	cggagtgggg gcnggaaat aanntattnn ggnnggaaan aaaaaaaaaa aaaaaaaaaa	710
	gcggccc	717
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FIGURE 8

5	tctagcgaac cccttcgccc agctgctaga agccaggctg gcctgggtgag gc atg agc	58
	Met Ser	
	1	
10	atg aag atg aac cca ggt gac aag gac aag atg ttg ctc ttc tcc cca	106
	Met Lys Met Asn Pro Gly Asp Lys Asp Lys Met Leu Leu Phe Ser Pro	
	5 10 15	
15	ccc ttt gac ccc tgt ctt cta agg cat cta gga agg aac cag tgt cct	154
	Pro Phe Asp Pro Cys Leu Leu Arg His Leu Gly Arg Asn Gln Cys Pro	
	20 25 30	
	tgg tac tga tttacttaga ttcaacctaa ggggccagcc actgactaag	203
	Trp Tyr *	
	35	
20	gccaaaggcca tttttccata cctgggaggg tagagattca gggttgtggg taagtgggca	263
	ctaaacatgg atttgcaagg gaaaacgaca gggcatcgag cttaaatttga atttacctga	323
	aattctgaaa tgtacttgta tgaagaaact gttatctgaa acctaaactta aatgggcctc	383
	ctgcctttttg tctggtgaga aatgaaagtg atctacaata agtgtcaaag caacaaggcc	443
25	cctctggata tgtctaggcc aggatgagga tactaagtgc cttcaaagcg agagggaggc	503
	aggccaagaa cactgcccta ctgaaaggca ggcttggccg gctagggcct ccaaggccct	563
	gatccctgag gcaccacagc cacaacttgt gtaggcctgg ccagggtcag tgaataggtt	623
	ctaggcagtg gttctcaacc ttctaattgc tgcaaccctt caatacagtt tctcctgttg	683
	tagtaatccc caaccataaa attatttttca ttgcgacttc ataactggac ttttgctact	743
30	gttatgaatc ataatgtaaa tatttttttg agctagaggt ttaccaaggg ggttgtgagc	803
	cataggttga aaaccattgt tctaggaata gctccagggg tggttttctga ggcccccgca	863
	agggtgggatc tatggggcag ggttggatct tctccaagag cccccaacag gatatatata	923
	tatatatata tatatatata tatatatata tatatatata tacttttgata gcatcccatg	983
	gaacgactgt ctctgatac taaagggagc ttggaagaaa ccaaggctga gagaagttgt	1043
35	agagtgggaa ggtaggcgaa gggattgagg tgacacagtg atagcccctt cagggtgggg	1103
	tctaccnag acagcagata aaggccttag gatgggagat tactctggct gctcagaggg	1163
	gaacacaggg acacagcacc aataaaatct ctttcttttc aaaaaaaaaa aaaaaaaaaa	1223
	aaaaagcggn cc	1235
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FIGURE 9

5	tctagcgaac	ccottcgatt	ttattagctc	ttgctttctcc	attcctcata	atztatgaat	60
	tatacagcct	togettgaa	acgcgtctga	agttatgctt	tgtgttggtg	tgggtttttt	120
	tttttttttc	ttttcttttt	ttttggagct	ggggaccgaa	cccagggcct	tgttgctcta	180
	ccaactgagct	aaatccccaa	ccctgttgt	gtgttttaaa	taagtctctt	actgtccatt	240
	ttgtaattag	tgttggttacc	ttgtaataat	agacatcata	caaagtttcc	tcttttttgt	300
10	gccagtgtg	agaacatgag	aaacatttaa	tgagtatttg	tttgttaaat	aatatttata	360
	acggctagaa	tggcagacac	ac atg gta	gca cat gat	ggt gat ttt	cgg ggg	412
			Met Val Ala His Asp Gly Asp Phe Arg Gly				
			1	5		10	

15	cct ttt gtt tgc tca gag ctg gta atc tct gcc ggt tgg ttt gct ttg	460
	Pro Phe Val Cys Ser Glu Leu Val Ile Ser Ala Gly Trp Phe Ala Leu	
	15 20 25	

20	cct ggt ctg gga cta acc tca cat ttt ctc act ctt gct ttc cga gag	508
	Pro Gly Leu Gly Leu Thr Ser His Phe Leu Thr Leu Ala Phe Arg Glu	
	30 35 40	

25	att agt cat cct tcc tgt cct act ggg ctc tcg ata gcg ctc atc agc	556
	Ile Ser His Pro Ser Cys Pro Thr Gly Leu Ser Ile Ala Leu Ile Ser	
	45 50 55	

30	ata ctg cat ttc aat ccc agc gaa ggg gtt cgc cga agg ggt tcg cta	604
	Ile Leu His Phe Asn Pro Ser Glu Gly Val Arg Arg Arg Gly Ser Leu	
	60 65 70	

35	ggc cag tgt gat gga tat ctg cag aat tc	633
	Gly Gln Cys Asp Gly Tyr Leu Gln Asn	
	75 80	

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FIGURE 10

5	tctagcgaac ccttcgcct ttctccaaag ccttcccggtt tctctttgac agctacgggc	60
	tgaggcagcc attcctgcag cagcgctcgg ccggtgaagg gccgaactga cgctcctag	120
	atctgtctcg gctgaattac tctcaccgt ttcattctg tgtgcaccag aaatctgaga	180
	tccaggagta tcaacagcaa ag atg tct aat gag cca ccc cct cct tat cca	232
	Met Ser Asn Glu Pro Pro Pro Pro Tyr Pro	
10	1 5 10	
	gga ggg cct aca gcc cca cta ctg gag gaa aaa agt gga gcc cca cat	280
	Gly Gly Pro Thr Ala Pro Leu Leu Glu Glu Lys Ser Gly Ala Pro His	
	15 20 25	
15	acc cca ggc cga acc ttt cca gct gtg atg cag cca cca cca ggc atg	328
	Thr Pro Gly Arg Thr Phe Pro Ala Val Met Gln Pro Pro Pro Gly Met	
	30 35 40	
20	cca ctg ccc tct gtt gac att gcc ccc ccg ccc tat gag ccg cct ggc	376
	Pro Leu Pro Ser Val Asp Ile Ala Pro Pro Pro Tyr Glu Pro Pro Gly	
	45 50 55	
	cat cca ggg cct aag cct ggt ttw atg ccc ccc acn tta cca cac att	424
25	His Pro Gly Pro Lys Pro Gly Xaa Met Pro Pro Thr Leu Pro His Ile	
	60 65 70	
	cna ana acc ttn ntn tgt aaa agt taa ataanaangg agggattcga	471
	Xaa Xaa Thr Xaa Xaa Cys Lys Ser *	
30	75 80	
	ccccctnca acnggtttca agccaattty mtaaccatit tgtttttttc wtttaaaaaa	531
	aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggaaaaaaaa aaaaaaaaaa	591
	aaaaaagggg ggcccc	607
35		
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50		
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FIGURE 11

5	tctagcgaac cccttcgcaa agtcctaagc cttac atg aga aaa ttt aag aca	53
	Met Arg Lys Phe Lys Thr	
	1 5	
10	ccc tta atg att gcg gaa gaa aaa tac aga caa caa agg gaa gag ctt	101
	Pro Leu Met Ile Ala Glu Glu Lys Tyr Arg Gln Gln Arg Glu Glu Leu	
	10 15 20	
15	gag aaa cag aga cgg gag agt tct tgc cat agc atc atc aaa aca gaa	149
	Glu Lys Gln Arg Arg Glu Ser Ser Cys His Ser Ile Ile Lys Thr Glu	
	25 30 35	
20	acc cag cac cgc agc tta tca gag aaa gag aaa gaa aca gag tta caa	197
	Thr Gln His Arg Ser Leu Ser Glu Lys Glu Lys Glu Thr Glu Leu Gln	
	40 45 50	
25	aaa gca gct gag gca atg tcc act ccc aga aag gat tca gac ttc act	245
	Lys Ala Ala Glu Ala Met Ser Thr Pro Arg Lys Asp Ser Asp Phe Thr	
	55 60 65 70	
30	agg gca cag ccc aac ctg gaa cct aaa agc aag gct gtg atc gcc agt	293
	Arg Ala Gln Pro Asn Leu Glu Pro Lys Ser Lys Ala Val Ile Ala Ser	
	75 80 85	
35	gaa tgc tct gaa agc cag ctc tct aca gct tcc gca ttg aca gtc gct	341
	Glu Cys Ser Glu Ser Gln Leu Ser Thr Ala Ser Ala Leu Thr Val Ala	
	90 95 100	
40	acc gag agg ctc cag cat gtt cta gcc gct tca gac gat aag ctt acc	389
	Thr Glu Arg Leu Gln His Val Leu Ala Ala Ser Asp Asp Lys Leu Thr	
	105 110 115	
45	ctg cga cgg gaa ggc aca cag aac tca agt gac acc cta caa tcg aaa	437
	Leu Arg Arg Glu Gly Thr Gln Asn Ser Ser Asp Thr Leu Gln Ser Lys	
	120 125 130	
50	aca gct tgt gag att aac cag agt cac aag gaa tgt agg aca gag caa	485
	Thr Ala Cys Glu Ile Asn Gln Ser His Lys Glu Cys Arg Thr Glu Gln	
	135 140 145 150	
55	aca ttt gag caa cac gtg gag aag ttg ccc ttc ccc caa acc aaa ccc	533
	Thr Phe Glu Gln His Val Glu Lys Leu Pro Phe Pro Gln Thr Lys Pro	
	155 160 165	
60	att tcc ccg agt ttc aaa gtg aaa act atc agg ctt cca gct cta gat	581
	Ile Ser Pro Ser Phe Lys Val Lys Thr Ile Arg Leu Pro Ala Leu Asp	
	170 175 180	
65	cat acg ctg act gaa aca gat ctc agt tct gaa cgc cgc gta aag caa	629
	His Thr Leu Thr Glu Thr Asp Leu Ser Ser Glu Arg Arg Val Lys Gln	
	185 190 195	
70	tcc gaa att gac gtt caa acc agt act aaa gaa atg aat aag gaa att	677

Ser Glu Ile Asp Val Gln Thr Ser Thr Lys Glu Met Asn Lys Glu Ile
 200 205 210

FIGURE 11 (cont.)

5	aag aaa acc gaa gtg agc aca cag tgt gat aat aag caa tct gtg gct Lys Lys Thr Glu Val Ser Thr Gln Cys Asp Asn Lys Gln Ser Val Ala 215 220 225 230	725
10	gaa aaa tat ttt caa tta cct aaa aca gag aaa cgg gtg acg gta caa Glu Lys Tyr Phe Gln Leu Pro Lys Thr Glu Lys Arg Val Thr Val Gln 235 240 245	773
15	atg ccc aaa gac tat gca gcg aaa agt cat caa agc aaa ctc caa aca Met Pro Lys Asp Tyr Ala Ala Lys Ser His Gln Ser Lys Leu Gln Thr 250 255 260	821
20	gtt ccc aag aag cat gga gga ttg ggg gag ttt gac aga ggg aat gtc Val Pro Lys Lys His Gly Gly Leu Gly Glu Phe Asp Arg Gly Asn Val 265 270 275	869
25	ctg ggg agg gaa gga aaa aat cag gac tcc tcc atg agc agt aca aaa Leu Gly Arg Glu Gly Lys Asn Gln Asp Ser Ser Met Ser Ser Thr Lys 280 285 290	917
30	gaa agc agg gta ata gtt gaa aga aag caa gaa cat cta cag gac cag Glu Ser Arg Val Ile Val Glu Arg Lys Gln Glu His Leu Gln Asp Gln 295 300 305 310	965
35	agc gta cca agg tta gtc caa caa aag att atc ggt gaa agc ctg gac Ser Val Pro Arg Leu Val Gln Gln Lys Ile Ile Gly Glu Ser Leu Asp 315 320 325	1013
40	tca cgg gtt cag aat ttt cag cag aca caa aca caa act tct agg att Ser Arg Val Gln Asn Phe Gln Gln Thr Gln Thr Gln Thr Ser Arg Ile 330 335 340	1061
45	gag cat aaa gaa ctg tcc caa cct tac agt gag aaa aaa tgt ctt aga Glu His Lys Glu Leu Ser Gln Pro Tyr Ser Glu Lys Lys Cys Leu Arg 345 350 355	1109
50	gac aag gac aaa caa caa aaa cag gtc tcc tct aac act gac gat tca Asp Lys Asp Lys Gln Gln Lys Gln Val Ser Ser Asn Thr Asp Asp Ser 360 365 370	1157
55	aag caa gag ata aca caa aaa caa tct tca ttt tcc tct gtg aga gaa Lys Gln Glu Ile Thr Gln Lys Gln Ser Ser Phe Ser Ser Val Arg Glu 375 380 385 390	1205
60	tcc cag cag gat gga gaa aaa tgt gcc ata aaa ata ttg gaa ttc ttg Ser Gln Gln Asp Gly Glu Lys Cys Ala Ile Lys Ile Leu Glu Phe Leu 395 400 405	1253
65	aga aaa cgt gaa gaa cta cag cag att ttg tct agg gta aaa cag ttt Arg Lys Arg Glu Glu Leu Gln Gln Ile Leu Ser Arg Val Lys Gln Phe 410 415 420	1301
70	gaa gca gat tca aat aaa agt ggc ctt aaa aca ttt cag aca ctg tta	1349

Glu Ala Asp Ser Asn Lys Ser Gly Leu Lys Thr Phe Gln Thr Leu Leu
 425 430 435

FIGURE 11 (cont.)

5 aat att gct ccg gtg tgg ctg ata agt gag gag aaa aga gaa tat gga 1397
 Asn Ile Ala Pro Val Trp Leu Ile Ser Glu Glu Lys Arg Glu Tyr Gly
 440 445 450

gtt cgt gtt gcc atg gag aat aat tag aaaaaataaa aaaaaaaaaa 1444
 10 Val Arg Val Ala Met Glu Asn Asn *
 455 460

aaaagcggcg nc 1456

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FIGURE 12

5	gaattgtaat acgactcact atagggcgaa ttgggcccct agcgaacccc ttcgacaaca	60
	tcaaagagga cagatctaac cctagactga ggccggaggc ctggaccaat tacctgaggg	120
	atgtccacag agcctttgca ctgctgaaca gtcaccctga tccaaaccaa gtaaattggga	180
	ctccaactgc accaagcagt ggccctcccag tcacctctgc tgagctcttg gtgccggcag	240
	ag atg gct tct gca gag tca ggt gaa gac cca agt cat gtg gtt ggg	287
10	Met Ala Ser Ala Glu Ser Gly Glu Asp Pro Ser His Val Val Gly	
	1 5 10 15	
	gaa acg cct cct ttg acc ttg cca gcc aac ctc caa acc ctg cat ccg	335
15	Glu Thr Pro Pro Leu Thr Leu Pro Ala Asn Leu Gln Thr Leu His Pro	
	20 25 30	
	aac aga cca acg ttg agt cca gag aga aaa ctt gaa tgg aat aac gac	383
	Asn Arg Pro Thr Leu Ser Pro Glu Arg Lys Leu Glu Trp Asn Asn Asp	
	35 40 45	
20	att cca gaa gtg aat cgt ttg aat tct gaa cac tgg aga aaa act gag	431
	Ile Pro Glu Val Asn Arg Leu Asn Ser Glu His Trp Arg Lys Thr Glu	
	50 55 60	
25	gag cag cca gga cgg ggg gag gtg ctt ctc ccc gaa ggt gac gtc agt	479
	Glu Gln Pro Gly Arg Gly Glu Val Leu Leu Pro Glu Gly Asp Val Ser	
	65 70 75	
	ggc aac ggt atg aca gag ctg ttg ccc atc ggt cgg cac caa caa aag	527
30	Gly Asn Gly Met Thr Glu Leu Leu Pro Ile Gly Arg His Gln Gln Lys	
	80 85 90 95	
	cgt ccc cac gat gcg ggg cca gag gac cat gct ttt gaa gat caa ttg	575
35	Arg Pro His Asp Ala Gly Pro Glu Asp His Ala Phe Glu Asp Gln Leu	
	100 105 110	
	cat cct ctc gtc cac tct gac aga act ccc gtt cat cgg gtg ttc gat	623
	His Pro Leu Val His Ser Asp Arg Thr Pro Val His Arg Val Phe Asp	
	115 120 125	
40	gtg tcc cac ttg gag cag cct gtt cac tcc agc cac gtg gaa gga atg	671
	Val Ser His Leu Glu Gln Pro Val His Ser Ser His Val Glu Gly Met	
	130 135 140	
45	ttg gcc aag atg gag ggg atg gca caa agg agt ggg cac caa gtc tcg	719
	Leu Ala Lys Met Glu Gly Met Ala Gln Arg Ser Gly His Gln Val Ser	
	145 150 155	
	aag gca gcg cct cct ctc cag tca ctt ctt gct tag attacatgtt	765
50	Lys Ala Ala Pro Pro Leu Gln Ser Leu Leu Ala *	
	160 165 170	
	gcctaacaat gtttctttcc atgttttgat tagtaaaacta actcgtggtg gcaatcatga	825
	ctcccaacct tctgagctcc ccggggtacg cttgcaccgt agacgctcat gtgcgcaccg	885
55	tgogggtgat gctcacacac agactcattg taattcaccg ttttaccgag aagggggggg	945
	gggcgaattt tctgtgttga tgctttgttt ttggtactaa aacagnatta tcttttgaat	1005
	attgtagggga catgagtata taaagtctat ccagtcacaaa tggctagaat tgngcctttg	1065

FIGURE 13

5	tctagcgaac cccttcgggg gttttcatc	atg gag ctg tcg cgg cgg att tgt	53
		<u>Met Glu Leu Ser Arg Arg Ile Cys</u>	
		-25 -20	
10	ctc gtc cga ctg tgg ctg ttg cta ctg tca ttc tta ctg ggc ttc agc		101
	<u>Leu Val Arg Leu Trp Leu Leu Leu</u>	<u>Leu Ser Phe Leu Leu Gly Phe Ser</u>	
	-15	-10 -5	
15	gcg gga tct gcc ctc aac tgg cgg gaa caa gaa ggc aag gaa gta tgg		149
	<u>Ala Gly Ser Ala Leu Asn Trp Arg</u>	<u>Glu Gln Glu Gly Lys Glu Val Trp</u>	
	1	5 10	
20	gat tac gtg act gtt cga gag gat gca cgc atg ttc tgg tgg ctc tac		197
	<u>Asp Tyr Val Thr Val Arg Glu Asp Ala Arg Met Phe Trp Trp Leu Tyr</u>		
	15	20 25 30	
25	tat gcc acc aac cct tgc aag aac ttc tca gag ctg cct ctg gtc atg		245
	<u>Tyr Ala Thr Asn Pro Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met</u>		
		35 40 45	
30	tgg ctt cag ggt ggt cca ggt ggt tct agc act gga ttt gga aac ttt		293
	<u>Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe</u>		
		50 55 60	
35	gag gaa atc ggc cct ctt gac acc cga ctc aag cca cgg aac act acc		341
	<u>Glu Glu Ile Gly Pro Leu Asp Thr Arg Leu Lys Pro Arg Asn Thr Thr</u>		
		65 70 75	
40	tgg ctg cag tgg gcc agt ctc ctg ttc gtg gac aat cct gtg ggc acg		389
	<u>Trp Leu Gln Trp Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr</u>		
	80	85 90	
45	ggc ttc agt tac gtg aac acg aca gat gcc tac gca aag gac ctg gac		437
	<u>Gly Phe Ser Tyr Val Asn Thr Thr Asp Ala Tyr Ala Lys Asp Leu Asp</u>		
	95	100 105 110	
50	acg gtg gct tcc gac atg atg gtc ctc ctg aaa tcc ttc ttt gat tgt		485
	<u>Thr Val Ala Ser Asp Met Met Val Leu Leu Lys Ser Phe Phe Asp Cys</u>		
		115 120 125	
55	cat aaa gaa ttc cag acg gtt ccg ttc tac att ttc tca gaa tcc tac		533
	<u>His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu Ser Tyr</u>		
		130 135 140	
60	gga gga aag atg gct gct ggc atc agt tta gaa ctt cac aag gct att		581
	<u>Gly Gly Lys Met Ala Ala Gly Ile Ser Leu Glu Leu His Lys Ala Ile</u>		
	145	150 155	
65	cag caa ggg acc atc aag tgc aac ttc tct ggg gtt gct ttg ggt gac		629
	<u>Gln Gln Gly Thr Ile Lys Cys Asn Phe Ser Gly Val Ala Leu Gly Asp</u>		
	160	165 170	
70	tcc tgg atc tcc cct gtg gat tca gtg ctg tcc tgg gga cct tac ctg		677

Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro Tyr Leu
 175 180 185 190

FIGURE 13 (cont.)

5	tac agc gtg tct ctc ctt gat aat aaa ggc ttg gct gag gtg tcc gac	725
	Tyr Ser Val Ser Leu Leu Asp Asn Lys Gly Leu Ala Glu Val Ser Asp	
	195 200 205	
10	att gcg gag caa gtc ctc aat gaa aaa caa ggg ctt cta caa gga agc	773
	Ile Ala Glu Gln Val Leu Asn Glu Lys Gln Gly Leu Leu Gln Gly Ser	
	210 215 220	
15	cac tca gct gtg ggg gaa agc aga aat gat cat tga aaagaacacc	819
	His Ser Ala Val Gly Glu Ser Arg Asn Asp His *	
	225 230	
20	gacggggtaa aottctataa catcttaact aaaagcaccc ccgacacctc tatggagtcg	879
	agcctcgagt tttccggag ccccttagtt cgtctctgtc agcgccacgt gagacaccta	939
	caaggagacg ccttaagtca gtcctatgaac ggtcccatca aaaagaagct caaaattatc	999
	cctgacgacg tctcctgggg agcccagtcg tcctccgtct tcataagcat ggaagaggac	1059
	ttcatgaagc ctgtcatoga catcgtggat acgttgctgg aactcggggg caatgtgact	1119
	gtgtacaatg ggcagctgga tctcattgtg gacaccatag gtcaggagtc ctgggttcag	1179
	aagctgaagt ggccacagct gtccagattc aatcagctaa aatggaaggc cctgtacacc	1239
	gacctaagt cttcagaaac atctgcattt gtcaagtcct atgagaacct agcgttctac	1299
25	tggatcctaa aggcgggtca catggttccct gctgaccaag gggacatggc tctgaagatg	1359
	atgaggctgg ttactcagca ggagtagctg agctgagctg gccctggagg ccctggaggc	1419
	cctggagtag ggcccaggat gcaggtgcta atgtctatcc ccggcgctct tcttccgac	1479
	tctaccatgg gatgtaactc caggagcccc tgccatctcc cgtaccaaaa gactgtggct	1539
	tccgtgtcta ctcagaaatc agttctactt cgtaaacagt gtttaaaacc agactcattt	1599
30	aatcagagtg aaggattgca gtccattggc ttcttagcac agaagcagct gataacacaa	1659
	gtaaacccca gcccttgaga ggtagaagca agaggatcag aggttcaagc gcatcctcgg	1719
	ctccatcaca agttcaaaaag ccgcctgcac caaatgggag tccttgtctc aaaaaaaaaa	1779
	aaaaaaaaaa aaaaagcggc cgc	1802
35		
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FIGURE 14

5	tctagcgaac cccttcgcga aggggttcgc taggttgcgt ttgtggagaa aaatctgttc	60
	tacctcaggg ctgtgagaac ggcactcctg atg tct gag aaa gag aaa caa gat	114
	Met Ser Glu Lys Glu Lys Gln Asp	
	1 5	
10	tgg ctg aag gat cct ccg ttc ctt cag aga cct ggg tgg aga gca tta	162
	Trp Leu Lys Asp Pro Pro Phe Leu Gln Arg Pro Gly Trp Arg Ala Leu	
	10 15 20	
	ggg aca cga aga aca gag tag cggaagaaga gttcttaagt aataagttta	213
15	Gly Thr Arg Arg Thr Glu *	
	25 30	
	cctcctgact ggctcacatc actgccttac tctgtagaaa gcaggtcatc tcatggattt	273
	ccccctccca cccccccagc tggatcattt tttgactcag ggaaaataat taaattattg	333
20	tccaaactggt agtggttgatc ggtaacagca gaaaggcaga aagttcctga taatctcaat	393
	attatctttt caaaagtatt ttcttggaat gttgtttgct ttggcattac aaagttctgt	453
	actcttaaaa atattttgac ttgctgggca tggaggtcac acctttaatc cagaggcagg	513
	catggatcca caggagttca aggcgcctg gctacaaagc gagttcaagg gcagccaggg	573
	ctacacagag agaccttgtc tentnaccnn tnannaaaaa acnaaaaagc cggccgc	630
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FIGURE 15

5	tctagcgaac cccttcggta tagtctttag gtagtggett agtccctgga agctctgggt	60
	gcttggcatt tcaacgtgct tcttaaataa ctgttttatt agtcagtaca ag atg ctt	118
	Met Leu	
	1	
10	tgt ata tca gat ctg aaa tat ctt aaa att atc act tgc att gta aat	166
	Cys Ile Ser Asp Leu Lys Tyr Leu Lys Ile Ile Thr Cys Ile Val Asn	
	5 10 15	
15	tac tat tcc ttt cgc aga aat aat gaa tgc ttc aag aaa aaa aaa agc	214
	Tyr Tyr Ser Phe Arg Arg Asn Asn Glu Cys Phe Lys Lys Lys Lys Ser	
	20 25 30	
20	tgt ttg tat tgg gtt taa aacgtttcca aacaccaatt attctttact	262
	Cys Leu Tyr Trp Val *	
	35	
25	taagtcaccc gatctagtta ttaaattatt attactgcct tcacactatc aaagatggta	322
	aatatctgat agaatcatat tcaaaaatact tctgtttcac atttcttgag aaagtactga	382
	ctgtctgagt tctttctcaa gaaatgtgaa acagaagtat tttgaatcga aggggttcgc	442
	tag	445
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FIGURE 16

5 tctagcgaac cccttcggaa gaactgtata tttgtgcctt gttctgcaag ttaaaaagct 60
ggtccagaca gtgtcataga attaacittt catttctgta ttaatttttag gactgcaaaa 120
atcccaaagc tgtatactta gattggattc aataaaaagt ttaagtttac tnaanaaaaa 180
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaanaaaaa aaaaaaaaagg 240
aaaaaaaaaa ncggncnnaa aaaaggnggc cgc 273

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FIGURE 17

5	tctagcgaac cccttcgggg gaacccaagc ggcttcgccc aggcattcgc gcgggcgccc	60
	gcgggtctggg tcccacctcc tctgctttcg cacccttgaa gttttggagc accaggaaaa	120
	gagggcaagg aaggagaggg gaagcgaaag catatcctaa aacatttact taaaggagga	180
	aagaaaaggg gtcgcagaa atg gct ggg gca att ata gaa aac atg agc acc	232
	Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr	
10	1 5 10	
	aag aag ctc tgc att gtt gga ggg att ctt ctg gtt ttc caa atc gtt	280
	Lys Lys Leu Cys Ile Val Gly Gly Ile Leu Leu Val Phe Gln Ile Val	
	15 20 25	
15	gcc ttt ctg gtg gga ggc ttg atc gct cca gca ccc aca acg gca gtg	328
	Ala Phe Leu Val Gly Gly Leu Ile Ala Pro Ala Pro Thr Thr Ala Val	
	30 35 40	
20	tcc tac gtg gca gca aaa tgt gtg gat gtc cgg aag aac cac cat aaa	376
	Ser Tyr Val Ala Ala Lys Cys Val Asp Val Arg Lys Asn His His Lys	
	45 50 55	
	aca aga tgg ctg atg ccc tgg gga cca aac aag tgt aac aag atc aat	424
25	Thr Arg Trp Leu Met Pro Trp Gly Pro Asn Lys Cys Asn Lys Ile Asn	
	60 65 70 75	
	gac ttc gaa gaa gca att cca agg gaa att gaa gcg aat gac att gtg	472
	Asp Phe Glu Glu Ala Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val	
	80 85 90	
30	ttt tct gta cac att ccc ctc cct tct atg gag atg agc cca tgg ttc	520
	Phe Ser Val His Ile Pro Leu Pro Ser Met Glu Met Ser Pro Trp Phe	
	95 100 105	
35	cag ttt atg ctg ttt atc ctg cag ata gac att gct ttc aag cta aac	568
	Gln Phe Met Leu Phe Ile Leu Gln Ile Asp Ile Ala Phe Lys Leu Asn	
	110 115 120	
40	aac caa atc aga gaa aat gca gaa gtt tcc atg gat gtt tcc ctg ggt	616
	Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Gly	
	125 130 135	
	tac cgt gat gat atg ttt tct gag tgg act gaa atg gcg cac gaa aga	664
45	Tyr Arg Asp Asp Met Phe Ser Glu Trp Thr Glu Met Ala His Glu Arg	
	140 145 150 155	
	gta cca cgt aaa ctc aga tgc act ttc aca tcc ccc aag acc cca gag	712
	Val Pro Arg Lys Leu Arg Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu	
	160 165 170	
50	cat gaa ggt cgt cat tat gaa tgt gat gtc ctt cct ttc atg gaa att	760
	His Glu Gly Arg His Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile	
	175 180 185	
55	ggg tca gtg gct cat aag tat tac ctt cta aat atc cgg cta cct gta	808
	Gly Ser Val Ala His Lys Tyr Tyr Leu Leu Asn Ile Arg Leu Pro Val	

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FIGURE 17 (cont.)

5	aat gag aag aag aaa atc aat gtt gga att ggg gaa ata aag gac att Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile 205 210 215	856
10	cgg ttg gtg gga atc cac caa aat gga ggt ttc act aag gta tgg ttt Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe 220 225 230 235	904
15	gct atg aag acc ttc ctc aca ccc agc atc ttc atc att atg gtg tgg Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp 240 245 250	952
20	tat tgg aga agg atc acc atg atg tcc cga cct cca gtg ctt ctg gaa Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu 255 260 265	1000
25	aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc aat atc cct Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro 270 275 280	1048
30	gtg gaa tgg ttt tcc att gga ttt gat tgg acc tgg atg ctg tta ttt Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe 285 290 295	1096
35	ggt gac ata cga cag ggc atc ttc tat gca atg ctt ctt tcc ttc tgg Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp 300 305 310 315	1144
40	atc atc ttc tgt ggc gag cac atg atg gat caa cat gag cgg aat cac Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His 320 325 330	1192
45	att gca ggg tat tgg aag caa gtt gga cca att gct gtt ggc tct ttc Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe 335 340 345	1240
50	tgc ctc ttc ata ttt gac atg tgt gag aga gga gtg caa ctc aca aat Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn 350 355 360	1288
55	cct ttc tac agt atc tgg act aca gat gtt gga aca gaa ctg gct atg Pro Phe Tyr Ser Ile Trp Thr Thr Asp Val Gly Thr Glu Leu Ala Met 365 370 375	1336
60	gct ttc atc att gtg gca ggt atc tgc ctc tgc ctc tac ttc ctg ttt Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe 380 385 390 395	1384
65	ctg tgt ttc atg gta ttt caa gta ttc aga aac atc agt ggg aaa cag Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln 400 405 410	1432
70	tct agc ctc cca gcc atg agc aaa gtc cgg agg ctg cac tat gag ggt	1480

Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly
 415 420 425

FIGURE 17 (cont.)

5	ctg att ttc agg ttc aag ttc ctc atg ctg atc acc ttg gct tgt gct	1528
	Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala	
	430 435 440	
10	gcc atg act gtt atc ttc ttc att gtt agt cag gtg aca gaa ggc cat	1576
	Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His	
	445 450 455	
15	tgg aaa tgg ggt ggg gtc aca gtt caa gtg agc agt gct ttc ttc act	1624
	Trp Lys Trp Gly Gly Val Thr Val Gln Val Ser Ser Ala Phe Phe Thr	
	460 465 470 475	
20	gga atc tat ggg atg tgg aac ctg tat gtc ttt gct ttg atg ttc ttg	1672
	Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu	
	480 485 490	
25	tat gca cca tcc cat aag aac tat ggg gaa gac cag tct aat ggt gac	1720
	Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Asp	
	495 500 505	
30	ctg ggt gtc cac agc ggg gaa gaa ctg cag ctc act acc aca atc acc	1768
	Leu Gly Val His Ser Gly Glu Leu Gln Leu Thr Thr Thr Ile Thr	
	510 515 520	
35	cat gta gat gga ccg act gag atc tac aag ttg acc cgt aaa gaa gca	1816
	His Val Asp Gly Pro Thr Glu Ile Tyr Lys Leu Thr Arg Lys Glu Ala	
	525 530 535	
40	cag gag tag taggctatgg cattcatcct cagggcaggt gatgaagcca	1865
	Gln Glu *	
	540	
	agttgctggt gcatgctgac cctcatgaat atgctttcgt atctttatgt cccaggatca	1925
	ttttatcct gtcacgttta caagaacatt tctgacatgc atacgtttac ttttaccatg	1985
	tattagttac ttttatatct ctgtgataaa acaccatgag aaatacaatt tacagaagca	2045
	aaaaaaaaa aaaaaaaaaa aaaagcggcc gc	2077

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FIGURE 18

5	tctaacgaac cccttcggag cgatgga atg aga aag gcc cag aat gtg tta agt	54
	Met Arg Lys Ala Gln Asn Val Leu Ser	
	1 5	
10	ctg tgc agg gga agt gtc ctg agg gga ggg tct ttg gga ggg tcg aag	102
	Leu Cys Arg Gly Ser Val Leu Arg Gly Gly Ser Leu Gly Gly Ser Lys	
	10 15 20 25	
15	gcc agg atg gca aag tga aggtagctga ggttgcagtc ttgggtgccc	150
	Ala Arg Met Ala Lys *	
	30	
20	actgctgtgc atctgtcttg ttatctaccc ctactttggg ctgacaactg caggggttggg	210
	tgtaggctgt ctcactgcat gccgggaagc tggagaagct ccacgggaac attgagggcc	270
	atggctttga gacactgcag agcatccttg gtctctgtaa ccacgtcacc taaccctgac	330
	aattccagac ccttcttcca ttgtccttgt gaaccatttg ggcttatctt tccctcttag	390
	tcgcaagggg caaaccaagg gtcagtcaag tagatgactg tcaccttggg cctccccaga	450
	ctctgctgcc ggggttggga gaccaaagta gaaactgcca ctacaaggcc ccaggatgag	510
	gtctctgttc tgtggacctg ctccccagat acaggcctca gacccatagg acgtggccgg	570
25	tgtctcaggga caaccaatcc ccggcctcac tccatcgagt actgacttct ttctctagt	630
	ccttgggggt ctccatcctt cagttatggt atgaagaatc tatgcaaact gtataagctt	690
	ctgtcacca ataaacgctt tatttaaagc ttannnnnnn nnnnnnnnn nnnnnaagcg	750
	gncgc	755
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FIGURE 19

5	tctagcgaac cccttcgcag aaacccaaag ttacagacca gaccctaccc aacatccagt	60
	cagcaatcca gctggagaaa cgcttgag atg aca agg gac ttt cag aag caa	112
	Met Thr Arg Asp Phe Gln Lys Gln	
	1 5	
10	gcc ttg ata aga cag gaa aag cag aat tct aat aaa gat atg agg aaa	160
	Ala Leu Ile Arg Gln Glu Lys Gln Asn Ser Asn Lys Asp Met Arg Lys	
	10 15 20	
15	aat gac atg ggc ctt caa cct ctg cct gta ggg aag gac gca cac agt	208
	Asn Asp Met Gly Leu Gln Pro Leu Pro Val Gly Lys Asp Ala His Ser	
	25 30 35 40	
20	gca cca gga gtg aca gtc tct ggg aaa aac cac aaa aga act cag gca	256
	Ala Pro Gly Val Thr Val Ser Gly Lys Asn His Lys Arg Thr Gln Ala	
	45 50 55	
25	cct gac aag aaa cag aga att gat gtt tgt cta gaa agc cag gac ttt	304
	Pro Asp Lys Lys Gln Arg Ile Asp Val Cys Leu Glu Ser Gln Asp Phe	
	60 65 70	
30	cta atg aag aca aat act tcc aag gag tta aaa atg gca atg gag agg	352
	Leu Met Lys Thr Asn Thr Ser Lys Glu Leu Lys Met Ala Met Glu Arg	
	75 80 85	
35	tcc ttt aat cca gtc aac ctt tcc ctg act gtg gtg taa aagaaaatga	401
	Ser Phe Asn Pro Val Asn Leu Ser Leu Thr Val Val *	
	90 95 100	
40	ggacgccctt ctctccatct tccccctcctt cttctccttc caattgcgtc atctgaaatt	461
	gaatttcctc tcctcctcca ccacctataa tgctgtgcct gaaaaaaatg agtttcctcc	521
	ctcatcaccac acagagaagt caagggtga acttgagagc ctccaaccc tgctctctcc	581
	tccaccacca ggagatgaga aatctgatca ggaatgtcta ccaacatccc tacctcctcc	641
	ccctcccaca gctccatccc aaccagcaca tcttctttcc tcctctgttc tagaacatca	701
	cagtgaagca tttttacaac agtattcccg aaaagaaacc ttggactctc atcggcttca	761
45	ctcacaggct aaaatcctaa caggaaaatc accaccccca acactcccca aacccaaact	821
	tcccagagaga atcaaagcta agatgagcca ggattcacca agcgggtgaat tggaagatc	881
	tctgtcagat gtggaaatta aaactaccct ctcaaaggat cagaaaagtt cgctggtggc	941
	agaaagccgt gagcacacag aggccaagca agaagtattc cgaaaaagcc ttggaagaaa	1001
	acagctgtcc attagctctg caaactccct ctctcagaca gttccagaaa tcccagcacc	1061
	caaggaaaaa cagacagcac cccttggttaa atctcactca ttcccatcag gttcagaaca	1121
	acaaagtcct aagccttaca tgagaaaatt taagacaccc ttaatgattg cggaagaaaa	1181
	atacagacaa caaagggaag agcttgagaa acagagacgg gagagttctt gccatagcat	1241
	catcaaaaca gaaacccagc accgcagctt atcaaanntt aaaaaaaaaa aaannnagc	1301
	ggnccgcccg	1310
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FIGURE 20

5	tctagcgaac cccttcgctt tttttttttt tttttttttt ttttcccccc tttcctattt	60
	attaatgggg ggaagtatgt ttatgtggga tttatccact tcttttagat tctcctacct	120
	gttgatctgt aattattcct agtagtctct tagagttcctt agaagcatgc tgttaccgct	180
	aatatttcct tttggtttgg atcttactta aacatattgt ttccttactc tctttttcat	240
	cccagcttgt ctaactgaaa ggccagaccc aacttgatct atccctttta aacttc atg	299
10		Met
		1
	tct tgg cct gtt gat ttc tct gct cca ggt gtc acc gaa ggg gtt cgc	347
15	Ser Trp Pro Val Asp Phe Ser Ala Pro Gly Val Thr Glu Gly Val Arg	
	5 10 15	
	cta gcg aac ccc ttc gta aca gcc aag gtt ttt gag aca gag gtt tca	395
	Leu Ala Asn Pro Phe Val Thr Ala Lys Val Phe Glu Thr Glu Val Ser	
	20 25 30	
20	aca gca ttc ctg gag gag aca caa agg aca gat gag tca cat gaa gga	443
	Thr Ala Phe Leu Glu Glu Thr Gln Arg Thr Asp Glu Ser His Glu Gly	
	35 40 45	
25	tgg gag gag gga agg tgg ctg ttg ata ggt att ttg aga cac tct att	491
	Trp Glu Glu Gly Arg Trp Leu Leu Ile Gly Ile Leu Arg His Ser Ile	
	50 55 60 65	
	tga gtccctacaca acactcccc ctcccccaa accattttta tgtctattga	544
30	*	
	cctttcctct agtcatacag ggaaattcac agttacctac aaagaaccac taattgtaac	604
	aagtcaagag gaaacttatt ttgataatg actcattgaa gatgttttga aaatttaaaa	664
35	ataagctctg ttagcagaag tctgttngaa aagcangaag gaantgtttg tttattanat	724
	aaataaaaagg cggcgaggac aacaaaaaaa aaaaaaaaaa aagcggccgc	774
40		
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FIGURE 21

5	tctagcgaac cccttcgcga aggggttcgc cgaaggggtt cgcttcagga gttaatgtag	60
	acttgactta agcatcctga tttaaccaag a atg gtg gca cac aac ttt aac	112
	Met Val Ala His Asn Phe Asn	
	1 5	
10	ccc cat gct ggg gaa gca gag gca cac tta atc tgt gtg agt ccc agg	160
	Pro His Ala Gly Glu Ala Glu Ala His Leu Ile Cys Val Ser Pro Arg	
	10 15 20	
15	cca tcc agg gat acc gta gta gtg aga ccc tgt ctc aca aaa caa aga	208
	Pro Ser Arg Asp Thr Val Val Val Arg Pro Cys Leu Thr Lys Gln Arg	
	25 30 35	
	atg gga att tag ggctgggtggg gctcagcatg caactgtgcc tgttacctag	260
	Met Gly Ile *	
20	40	
	tctggcctga gttcaattcc caagactcaa tgtatgagga gagaaacgat ttctgaactc	320
	attcattgat ctccaaatgt gtggtatagg tgcccttccc ttaaataaaaa caaacaaaca	380
	aaaaacaaca aaaacaacaa accccaata aatgtatatt taattttaaa agactgtact	440
25	tgggcatggt acttcacatc tacagttacg acattctaga ggctcaggcc tgggaattgc	500
	tatgaatttg aggccagtct gggtttagagt gacttctcat ctaggcagga ctacgtaata	560
	agtctttgcc caaaaataaaa cagcaaccca aataagagca acaagaattc tccctccaaa	620
	tagtaacctg ggccctggaga gacagcttag caactgagtg cttgccgagc catcgaggac	680
	tggagtctgg attccagcac cagtgtgaca gacaagctgg gcgttcactc atgctgatga	740
30	acccaaggc tgaggagaca ctgactcttc tctggccctg ttcattgctgt ccacaggtgc	800
	ccaagtagca gttaagtaga ctgtcagaca acatggctgg ctttttaagc aagaacagta	860
	actgaagaaa tacacttttg aagtactgtt aattttgctt aaaacttggg agggagctgg	920
	aggatggctc agtgggttaag agcactgact gctcttcag aggtcctgag ttcaattccc	980
	agcaaccaca tgggtggctca caaccatctg taatgagctc tgatgccctc tttttggtgt	1040
35	gtctgaagac agcgacagtg tactcatata aaataaaata aatctttttt ttttttaaaa	1100
	gaaatttgtc agagatatgg caggaagggt atatttttac ctattttacct ggtgggctaa	1160
	tcctggtatt tttttcaaaa ttaagatact atataggagc cgcggaagggg tcgctaggcc	1220
	agtgtgatgg atatctgcag aattcgggta gccgaattc	1259
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FIGURE 22

5	tctagcgaac cccttcgtct cctctttaaac atcttaagac aagctgttat catctacact	60
	gctcttagta ctgttctttt ctaagattct tctaataatga cacattaaga ctttctttaa	120
	atgtacaact gctacgtga tctaaacatt caaagtgcac acatttcgct atgaagccac	180
	gtgaccagag tcttggggac taatttctgt cttagtcaga ttcctattgc tatatgaaga	240
	aatacc atg ata gtg tca act ttt ata aag aaa aag tat tcc ttt ggg	288
10	Met Ile Val Ser Thr Phe Ile Lys Lys Lys Tyr Ser Phe Gly	
	1 5 10	
	aat agt tta aag gat cag agg gtt agt gca tta tca tca cag cag gaa	336
	Asn Ser Leu Lys Asp Gln Arg Val Ser Ala Leu Ser Ser Gln Gln Glu	
15	15 20 25 30	
	gcg tgg cag tgg gag ccc aga ttt cta tat cca gat ttt cat gaa gca	384
	Ala Trp Gln Trp Glu Pro Arg Phe Leu Tyr Pro Asp Phe His Glu Ala	
	35 40 45	
20	tga cgagagctcc tgggcctggc gcgagcttct gaaacctgaa agtgacatat	437
	*	
25	ttcttccaat aaggccacaa ctactgotat aaggccacat ctcttaactg tgtcactatc	497
	tatgagcctg tacagtctat ttcttttaca ccactgcac atctaagagc tgatacccg	557
	taagttagtc atgaaaatat tcaacttcta gggttctgtt ttcttctcta taaaatattg	617
	aaaatgataa ttaatgtata ctttacagaa ctgtatttga agtacaactt gatggacata	677
	aatcaccaca gttgggtcaa aattgtatat atatatatat atatatatat atatatatat	737
30	atatatcaaa aaaaaaaaaa aaaaaaaaaa aagcggccgc	777
35		
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FIGURE 23

5	tctagcgaac	cccttcgtac	atttcacccct	agaaataaat	agaccttcta	gctctgacag	60
	aaagtagtgc	ttgcctagga	ggagctgggc	tggccagttc	ctccttcttg	cacacttagc	120
	ctgtttgtctg	aaggcttggt	tcaatggaaa	actgaaatgg	accactaat	gtctcgattc	180
	ttctctcctt	cactaagtct	gtgaagtcac	cagcgttttg	tcttttgtgt	gtgaataccg	240
	aggagaattt	cctcaccag	tgccttcagg	agccatgatg	gctgcctcag	aataagcaca	300
10	gatacacttg	agcaactggt	gcagaaaacc	cgacttctaa	attattaagg	aacaggataa	360
	ttgcttggtta	caataattag	aataatgtaa	ttaggataat	tgcttttaaa	aaatcttccc	420
	acctttcccc	ccccaaatat	taataattcc	aactaaatcc	tctggggccc	ttccagtttc	480
	cacaacggaa	agagcctaac	gtattctaaa	gactgggcat	atTTTTTTTT	tccagattag	540
	tgagtgttca	tgagctatta	agaggccaag	tgTTTTTTTca	agatgggtgtc	atttcattct	600
15	aacatatcta	acatgcaaag	gacttaaaaa	aataatttgc	aaaataatct	gtttcaagtc	660
	tatgaggaag	ctgaagagcc	tactccggag	gaaactccag	aagagcctcc	tagcatagag	720
	gaagaagaga	tagtgaggga	agaggaggag	gaggaggtgc	ccccgcccag	aggtacagcc	780
	gctttgatga	gttcagcatt	ccaaagcctt	ggtgctgtct	gacctactc	attagccata	840
	tactttcctg	gaagcacagc	cacgaggcct	ggagggtgca	cactcgtaat	gactggagct	900
20	ttgtgggcct	ttcctttccc	ctaacgtttc	ctccttcccc	gcaatctgac	cataaatgag	960
	gagatttttt	ttttctctta	ctaacgtttt	tgcaatccta	gtttgcaatc	ctcagtggtg	1020
	ctggcttttca	gttcaaatgc	tggagaacca	tgtatctgtg	tggtgagagc	attcattttc	1080
	aagactaatt	cttaaacccg	ttatccccgg	agacagaaac	cgtggcagag	ttgctatcct	1140
	ctgagctggg	gtgggtcatga	tgatcagtta	ggttactaac	atcttcctaa	atgaatcggt	1200
25	gttttgtgtt	gctctgtttt	catttggtatg	acagggtgtt	gttctgttta	atgctgtgtg	1260
	gtttttccaa	catgtccgta	aaaatatctt	ttaagcacca	gangtagtga	agaaagctgt	1320
	gcaaacagca	cccgctcctg	tccccagaa	awccgaggcg	cccccccaa	ggtatatc	1378

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FIGURE 24

5	tctagcgaac cccttcgcga accccttcgc tgcctcctca taaagctacc tcaagacaga	60
	gogtaactgc ctcattctag gagtggactc ggggaagaca gcagacacac catcagggag	120
	ccoctgggta tctccagaac atg gca agc cgt gga tac ctg cat cac ctg ctg	173
	Met Ala Ser Arg Gly Tyr Leu His His Leu Leu	
	1 5 10	
10	act gca gag gga gcc tgg gag gag ttt gta tca aag gcc aag ttg ccc	221
	Thr Ala Glu Gly Ala Trp Glu Glu Phe Val Ser Lys Ala Lys Leu Pro	
	15 20 25	
15	agg gat agg gca gtg gcc ctc cac aaa gca ctg agg gat ctg aca gca	269
	Arg Asp Arg Ala Val Ala Leu His Lys Ala Leu Arg Asp Leu Thr Ala	
	30 35 40	
20	ctc ttg gcc ata gca gaa aga ggc aga tct cgg aaa ggc ttg aaa ggc	317
	Leu Leu Ala Ile Ala Glu Arg Gly Arg Ser Arg Lys Gly Trp Lys Gly	
	45 50 55	
25	aag gag aag ttt gtg aaa gca ttt cct tgc ttg aaa gca gac ttg gag	365
	Lys Glu Lys Phe Val Lys Ala Phe Pro Cys Leu Lys Ala Asp Leu Glu	
	60 65 70 75	
30	gag cac atc agc cag ctc tat gcc cta gcc gac cat gct gag gaa ctg	413
	Glu His Ile Ser Gln Leu Tyr Ala Leu Ala Asp His Ala Glu Glu Leu	
	80 85 90	
35	cac agg ggc tgc acc gtc tcc aac atg gtg gct gac tcc ttc agt gtt	461
	His Arg Gly Cys Thr Val Ser Asn Met Val Ala Asp Ser Phe Ser Val	
	95 100 105	
40	gcc tcc gac atc ctg aac atc ttt ggt ctc ttt ctg gca cct gag tca	509
	Ala Ser Asp Ile Leu Asn Ile Phe Gly Leu Phe Leu Ala Pro Glu Ser	
	110 115 120	
45	gca gag gga agt ctg gtg ctc tgc gca gca ggc ttg ggg ctg ggg gta	557
	Ala Glu Gly Ser Leu Val Leu Ser Ala Ala Gly Leu Gly Leu Gly Val	
	125 130 135	
50	gca gct act gtg act aat gtt gct act tca atc atg aag gaa aca agc	605
	Ala Ala Thr Val Thr Asn Val Ala Thr Ser Ile Met Lys Glu Thr Ser	
	140 145 150 155	
55	agg gtt ttg gat gga gtc gaa gct ggt cac cat ggt tca acc gcc atg	653
	Arg Val Leu Asp Gly Val Glu Ala Gly His His Gly Ser Thr Ala Met	
	160 165 170	
60	gat ata ctg gag gaa gct ggc aca agt gtg gct agg att gcc agc gag	701
	Asp Ile Leu Glu Glu Ala Gly Thr Ser Val Ala Arg Ile Ala Ser Glu	
	175 180 185	
65	atc cct cag gct acc aga gat atc acc aga gac ctg gaa gcc ctt gag	749
	Ile Pro Gln Ala Thr Arg Asp Ile Thr Arg Asp Leu Glu Ala Leu Glu	
	190 195 200	

FIGURE 25

5	tctagegaac	cccttcggct	ttttctgatt	taaagtgaag	aaatggccat	atttgcttga	60
	taatcttcag	ttgtgtctct	ggaactcaac	aaagaacgca	ttttatgaaa	tatacagctg	120
	tcttcggtaa	agccaaacttt	cttacacata	tttcgggaag	taattaacta	caatttggac	180
	ttatagttac	aaggttgcct	tcgaaacact	gctctaaatg	tgtctcgtgt	tggggtgcta	240
	ctttgcttat	gtgtaaat	cacagtaatg	caatagagaa	aggggtgttg	tgggtgtggc	300
10	ttgtgggggg	gattgttttg	ttgttgttgt	ttgagataaa	gcttcattct	gtagccagga	360
	aagcctggaa	tttactgtgt	catcccaggt	agcttcaaac	tgggtgcctat	cctgcctcag	420
	cctccaacgt	gttgcaattg	caggagtaac	ctaccacatc	ctgcagctac	agtgatctag	480
	aacctccccg	tcgaagcccc	accaccatag	aaaccaat	gcattaagtt	ttagaattcc	540
	caaccaact	aaagtttaat	aaaaaaagaa	aaacaaaaca	agattttaa	cattctttcc	600
15	ctcattcttt	ttnnagatnc	agggctcncc	tagttttnaa	caaaacagtn	ngcagngnng	660
	ggnnccccng	gnggggnttt	tttncnttgn	gcncntnngc	anccccccn	cccaggcnng	720
	atngggnggg	gtataaaagt	nttanenggc	anatgnnctn	ggngcanacc	caagtntatc	780
	aggnccnana	ttncncacca	ganaactaga	nanctntnngc	atagtanang	ccccntgtgn	840
	agatttnaaa	ncncctgtgn	cacaganana	gaancttana	tagaaaantc	aaaatatttn	900
20	ggngcccaan	gttnccacc	ctgtagagng	ggccccaaa	ancngccncc	aganagcnng	960
	atatntgagt	tntgacctnt	attctttact	acnacgcntt	gagagaatat	tntgntgggg	1020
	ccctanccac	atgttttgnc	ccaagantgt	aaanccactt	naannctgng	ggatatctcn	1080
	ctgcanacag	aagtgccong	cgggatttta	aaaaaaaaa	taaaaaaaaa	aaaggngccn	1140
	cc						1142
25							
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FIGURE 26

5	tctagcgaac	ccttctgtgg	agactgtgga	agttatgtat	gaataggaga	gtgtgtggtg	60
	tgtaacacag	acagaaggac	attggatcat	gttgaaccgc	cacccccaac	tatgagtgat	120
	ggtatggaac	gaatgcgaac	atttaaactg	cgccaatgcg	gcggccatct	tggtggagaa	180
	gttcctatgc	gagctttgat	gtgatttttt	tgatggtaca	atgcagcgag	catggccacg	240
	ggagctttga	atccagccga	cagctccgag	atttgccctt	ccagtgtctt	tgctaccgtt	300
10	agagaggact	gctgagatgg	gattccttgt	gacaagccta	cttaccttta	actgccagca	360
	tttgtaaggt	gcaatcttgt	gtattggttt	tttattttga	cagttttgaa	aacatgtttg	420
	ntgntcttgg	tgtttttoca	gtaaaagtaa	tcacaaagga	aaaaaaaaatt	aaaaaaaaaa	480
	aaaaaaaaaa	aaaagcggcc	gc				502

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FIGURE 27

5	tctagcgaac	cccttcgcct	tcatatgggt	ttacactgta	tgcattctcac	cgcgggcccg	60
	aacctttctt	ctcatcccaa	tcctgtttga	ggggacgggg	ggcagggacg	gacaacccaa	120
	gacaagggat	atttgtgctg	tgggtattgc	atcttatgga	gggctgtagc	taactgggac	180
	tcctgggtga	ccccaacagg	cctttgatcc	tctgtctctc	cccgttgat	ctttcttacc	240
	ttatgcttcc	ccaagtgcag	ctgagggact	acacagtggc	tcccgcccca	ctccaaacac	300
10	aggaaatcaa	tctcagggag	aggagataag	aagtgaggag	aagccaagat	tcaaccaata	360
	gatggttaatt	gctcctggga	ccgccccccc	aagcatcatt	tccataggaa	ggactgagtt	420
	tggctcctga	agcccagtgg	agtacctttc	tctgcctgaa	ttctgttggtg	atccctggcc	480
	aagtccctctt	tccagaaacc	ccacctttaa	aaccagctga	gaaggacctt	cttctctatg	540
	tttaaataggt	aactttccat	agcttagctt	ccctgcagtc	tcccgagtgc	ccagttaaaa	600
15	ttctgccata	ggtcaaaagt	ggggttgaga	ggtgaagtca	gaggccatgc	atggagctca	660
	gaacgtttct	aaacctcctg	tgattcattg	agtagccct	agactctaga	aggctcagat	720
	gccaaaaagg	ktgactttat	aattttcttag	ggtcttctca	tgggatcgkt	ttcagagtgg	780
	gcattcacta	aatgatagca	agttttattaa	ttgtttccca	gygcctgatc	tctttatttn	840
	cccagggctt	ccaaccagag	cccttggttg	aaagtctccc	accaccccc	cacctgaga	900
20	cttggtggnt	ttctgagatt	ccccagggat	ggcaaaattg	gcattcttac	agggagccct	960
	gacttctagc	acgttaccta	gattttttac	cctgctctct	ctgcctattt	tactatggga	1020
	tactgntct	ctttggactt	aaggaaccac	cttgaagtag	agtgaggtga	ccacgtgttg	1080
	gtggcgaaga	atataagcat	tggtccttaa	aagagaactt	ctatgaagtc	aggctgcaag	1140
	ctttaacatg	gcacaagttg	caccttactg	gctgctaagt	ctggatgtca	accaaaggctc	1200
25	aactctntaa	ttaaagaaaa	gcaagggaga	aganagggtg	aagnggcttn	cataaaacttt	1260
	attcaaaaatg	tctaccagga	atggtggtga	caccaataat	cccacatggt	ggatgtngag	1320
	gcaggaagaa	tgatggtaag	gggcattctc	actacataat	gagttgaggc	tngactaggt	1380
	taactntgct	tnaaaaaaaa	aaaaaaaaaa	aaaaaaaaag	gnggcc		1426
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FIGURE 28

5	tctagcgaac ccttccgcaa gaactcagac tgctcctgcc tgacttccta ggtgtcatag	60
	ctctcttctg ccgccagt atg aca tca tca agg aca acg agc cca ata aca	111
	Met Thr Ser Ser Arg Thr Thr Ser Pro Ile Thr	
	1 5 10	
10	aca agg aaa aaa cca aga gtg cat cag aga cca gca ccc cag agc acc	159
	Thr Arg Lys Lys Pro Arg Val His Gln Arg Pro Ala Pro Gln Ser Thr	
	15 20 25	
	agg gtg ggg gtc tcc tcc gaa gca aga tat gaa acc ctt tca gtg ctt	207
15	Arg Val Gly Val Ser Ser Glu Ala Arg Tyr Glu Thr Leu Ser Val Leu	
	30 35 40	
	gct ctg agc agc tca gaa gta gaa tgc gag agg acc tca ctg ttc tga	255
	Ala Leu Ser Ser Ser Glu Val Glu Cys Glu Arg Thr Ser Leu Phe *	
20	45 50 55	
	cgatgattgt ccaacacaca tccggccctc tccgtgtctc ctcccaccac catcttctcc	315
	tatcaccggg cttactatct tctctcctgg ctttctctct tctgatggcg gttcctgaag	375
	cctccaacta acccctaact cggggagcgc ctcgacagtg tttgtggcta aggctacact	435
25	cagagacaga gttgcagaat gagggagacc cagcccaggg gacgccattg ctgggaggta	495
	gactgggtgc gagggccctt ggcacaggac tcacatctgg gctgttcagc ttgaccgaa	555
	ggctgtgtgt gaaaggggga aaaagacaag attgccaggc agggctgttg ttttgtggc	615
	ttcgagggac aagaacctgg ctaaaaggca gcagccctgc tgttcttttt ctctctgtc	675
	ctgtttccta cttacaaga agtccatgca accaaccggg gctctggcac ttttctgtt	735
30	tatttccctc ctggcttcca aacaagccct ctgtggacat catcaaagca tggataaccc	795
	cctctgcagg ggtgggcttc attctccgct ggtccctgta gccttctctg acacagggtg	855
	aaagttgtaa aagtggtagg agtgcagcta gccacagggt ctcttttcc catctcagtc	915
	tgaccaagga ggctgaaact ccaacccaaa ttcagcgaaa aaaaaaaaaa aaaaaaaaaa	975
	aagcggccgc	985
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FIGURE 29

5	tctagcgaac cccttcgcgg ggacagacat ggagaaggag atggaggacc ccctggctgg	60
	agcagaccaa cagaataggc aactatggct ggagaaccgg gtatcagagt aatgcttgac	120
	ctcgggaaac accaaatttc ttcttcgat cgcagaagta gtactcggcg aaattcacta	180
	ggtaggaggc tctcatctg ggaagaaccg gtgcctgggg ggacctggct ggataggt	238
	atg ggg gat cga ggc cgg tcc cct agt ctc cgg tcc ccc cat ggc agt	286
10	Met Gly Asp Arg Gly Arg Ser Pro Ser Leu Arg Ser Pro His Gly Ser	
	-35 -30 -25 -20	
	cct cca act cta agc acc ctc act ctc ctg ctg ctc ctc tgt gga cag	334
	Pro Pro Thr Leu Ser Thr Leu Thr Leu Leu Leu Leu Cys Gly Gln	
15	-15 -10 -5	
	gct cac tcc cag tgc aag atc ctc cgc tgc aat gcc gag tac gtc tcg	382
	Ala His Ser Gln Cys Lys Ile Leu Arg Cys Asn Ala Glu Tyr Val Ser	
	1 5 10	
20	tcc act ctg agc ctt cgg gga ggg ggc tca ccg gac acg cca cat gga	430
	Ser Thr Leu Ser Leu Arg Gly Gly Gly Ser Pro Asp Thr Pro His Gly	
	15 20 25	
25	ggc ggc cgt ggt ggg ccg gcc tca ggt ggc ttg tgt cgc gcc ctg cgc	478
	Gly Gly Arg Gly Gly Pro Ala Ser Gly Gly Leu Cys Arg Ala Leu Arg	
	30 35 40 45	
	tcc tac gct ctc tgc acg cgg cgc acc gcc cgc acc tgc cgc ggg gac	526
	Ser Tyr Ala Leu Cys Thr Arg Arg Thr Ala Arg Thr Cys Arg Gly Asp	
	50 55 60	
30	ctc gct ttc cac tcc gcg gtg cat ggc ata gag gac ctg atg atc cag	574
	Leu Ala Phe His Ser Ala Val His Gly Ile Glu Asp Leu Met Ile Gln	
	65 70 75	
35	cac aac tgc tca cgc cag ggt ccc acg gcc tcg ccc ccg gcc cgg ggt	622
	His Asn Cys Ser Arg Gln Gly Pro Thr Ala Ser Pro Pro Ala Arg Gly	
	80 85 90	
40	cct gcc ctg ccc ggg gcc ggc cca gcg ccc ctg acc cca gat ccc tgt	670
	Pro Ala Leu Pro Gly Ala Gly Pro Ala Pro Leu Thr Pro Asp Pro Cys	
	95 100 105	
45	gac tat gaa gcc cgg ttt tcc agg ctg cac ggt cga acc ccg ggt ttc	718
	Asp Tyr Glu Ala Arg Phe Ser Arg Leu His Gly Arg Thr Pro Gly Phe	
	110 115 120 125	
50	ttg cat tgt gct tcc ttt gga gac ccc cat gtg cgc agc ttc cac aat	766
	Leu His Cys Ala Ser Phe Gly Asp Pro His Val Arg Ser Phe His Asn	
	130 135 140	
55	cac ttt cac aca tgc cgc gtc caa gga gct tgg ccc cta cta gat aac	814
	His Phe His Thr Cys Arg Val Gln Gly Ala Trp Pro Leu Leu Asp Asn	
	145 150 155	
	gac ttc ctc ttt gtc caa gcc acc agc tcc ccg gta gca tcg gga gcc	862

Asp Phe Leu Phe Val Gln Ala Thr Ser Ser Pro Val Ala Ser Gly Ala
 160 165 170

FIGURE 29 (cont.)

5	aac gct acc acc atc cgg aag atc act atc ata ttt aaa aac atg cag	910
	Asn Ala Thr Thr Ile Arg Lys Ile Thr Ile Ile Phe Lys Asn Met Gln	
	175 180 185	
10	gaa tgc att gac cag aaa gtc tac cag gct gag gta gac aat ctt cct	958
	Glu Cys Ile Asp Gln Lys Val Tyr Gln Ala Glu Val Asp Asn Leu Pro	
	190 195 200 205	
15	gca gcc ttt gaa gat ggt tct gtc aat ggg ggc gac cga cct ggg ggc	1006
	Ala Ala Phe Glu Asp Gly Ser Val Asn Gly Gly Asp Arg Pro Gly Gly	
	210 215 220	
20	tcg agt ttg tcc att caa act gct aac ctt ggg agc cac gtg gag att	1054
	Ser Ser Leu Ser Ile Gln Thr Ala Asn Leu Gly Ser His Val Glu Ile	
	225 230 235	
25	cga gct gcc tac att gga aca act ata atc gtt cgt cag aca gct gga	1102
	Arg Ala Ala Tyr Ile Gly Thr Thr Ile Ile Val Arg Gln Thr Ala Gly	
	240 245 250	
30	cag ctc tcc ttc tcc atc agg gta gcg gag gat gtg gca cgg gcc ttc	1150
	Gln Leu Ser Phe Ser Ile Arg Val Ala Glu Asp Val Ala Arg Ala Phe	
	255 260 265	
35	tct gct gag cag gat cta cag ctg tgt gtt ggg gga tgc cct ccg agc	1198
	Ser Ala Glu Gln Asp Leu Gln Leu Cys Val Gly Gly Cys Pro Pro Ser	
	270 275 280 285	
40	cag cga ctc tct cgc tca gag cgc aat cgc cgt ggg gcg ata gcc ata	1246
	Gln Arg Leu Ser Arg Ser Glu Arg Asn Arg Arg Gly Ala Ile Ala Ile	
	290 295 300	
45	gat act gcc aga agg ttg tgt aag gaa ggg ctt ccg gtt gaa gat gcc	1294
	Asp Thr Ala Arg Arg Leu Cys Lys Glu Gly Leu Pro Val Glu Asp Ala	
	305 310 315	
50	tac ttc caa tcc tgc gtc ttt gat gtt tca gtc tcc ggt gac ccc aac	1342
	Tyr Phe Gln Ser Cys Val Phe Asp Val Ser Val Ser Gly Asp Pro Asn	
	320 325 330	
55	ttt act gtg gca gct cag tca gct ctg gac gat gcc cga gtc ttc ttg	1390
	Phe Thr Val Ala Ala Gln Ser Ala Leu Asp Asp Ala Arg Val Phe Leu	
	335 340 345	
60	acc gat ttg gag aac ttg cac ctt ttc cca gta gat gcg ggg cct ccc	1438
	Thr Asp Leu Glu Asn Leu His Leu Phe Pro Val Asp Ala Gly Pro Pro	
	350 355 360 365	
65	ctc tct cca gcc acc tgc cta gtc cgg ctt ctt tcg gtc ctc ttt gtt	1486
	Leu Ser Pro Ala Thr Cys Leu Val Arg Leu Leu Ser Val Leu Phe Val	
	370 375 380	
70	ctg tgg ttt tgc att cag taa gtaggcacgc aaccctgac tagtttggaa	1537

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Leu Trp Phe Cys Ile Gln *
385

FIGURE 29 (cont.)

5	acggtttgag	gagagaggtt	gatgtgagaa	aacacaaaga	tgtgccaaag	gaaacagtgg	1597
	ggacaggaga	caacgacctt	actcaatcac	acgaggttgc	agtccagggc	tgaaatgacc	1657
	ctagaataaa	gattctgaga	cagggttttg	cactccagac	cttggatatg	gctccccatg	1717
	aatttcccca	ttagtgattt	cccacttgta	gtgaaattct	actctctgta	cacctgatat	1777
	cactcctgca	aggctagaga	ttgtgagagc	gctaagggcc	agcaaaacat	taaagggctg	1837
10	agatatctta	aaggcagaaa	ctagaaaagg	ggaaaccatg	attatctata	agaaaatcaa	1897
	aagagggggt	tgggaattta	gctcagtggg	agagcacttg	cctagcaagc	gcaaggccct	1957
	gggttcgggc	cccagctcct	aaaaaaaaaa	aaaaaaaaaa	aaaaagcggc	cgc	2010

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FIGURE 30

5	tctagcgaac cccttcgtgg ggattaaggt tctctatagc taagcctgtc nga atg	56
	Met	
	1	
10	aca aca ccc aga gat ctc acc tgg ggt ggt ggg agc act ctc tgt ctt	104
	Thr Thr Pro Arg Asp Leu Thr Trp Gly Gly Gly Ser Thr Leu Cys Leu	
	5 10 15	
15	gag gga aca tgt acc tac tct ctc ctt cca caa gag cca cat aca ctt	152
	Glu Gly Thr Cys Thr Tyr Ser Leu Leu Pro Gln Glu Pro His Thr Leu	
	20 25 30	
20	aga agt tcc agt gaa gat cta tgt gct tca gaa gag agg gga ctt gga	200
	Arg Ser Ser Ser Glu Asp Leu Cys Ala Ser Glu Glu Arg Gly Leu Gly	
	35 40 45	
25	ggt gaa agg ggg agt ggg agg ggg gct tga ggacctanct gaaagatttt	250
	Gly Glu Arg Gly Ser Gly Arg Gly Ala *	
	50 55	
30	angctgaaag aacttccttg attcaaagac atatgtcagt ngaccaaca atgagaatga	310
	atatgagggc caggaaaact tgtgggaatc agtctcaaga cngaaacnga gaaagaaaga	370
	aaagtggnta ggactcanat tggggaacct gggtagacag gagtggcnag ggaagaaagg	430
	gatcttgggt tntccacagt ttgagacaca tccgngntc gacctattc ccngaagccn	490
	cannanatgt tgcttcccn tcnntnnaat gggcctggng gtcctnctcc ctttncccng	550
	gacatgaaaa ngtnnctgc nnanataacc cccntcttcc ccccccttn antntgtccc	610
	tacnnttttg tcccttttn ttttnaaaaa annaaaataa aggggnncnn tnttccttn	670
	gaaaaaaaaa aaaaaaaaaa aaaaaaccgc ccnc	705
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FIGURE 31

5	tctagegaac cccttcgcga aggggttcgc ttacattcac gcttaagcat attaaactgta	60
	catattaact gatttagagg atact atg gat tcc aca tct tcc ctg agc ata	112
	Met Asp Ser Thr Ser Ser Leu Ser Ile	
	1 5	
10	ggg att gat ttg aaa aat gac agg gtt ggc tgt cga ccc cca tcg gag	160
	Gly Ile Asp Leu Lys Asn Asp Arg Val Gly Cys Arg Pro Pro Ser Glu	
	10 15 20 25	
	gaa gca ggt aag gaa tca ctt agg aga act gat ctc aac att ctt cag	208
15	Glu Ala Gly Lys Glu Ser Leu Arg Arg Thr Asp Leu Asn Ile Leu Gln	
	30 35 40	
	ttc ttt cta tta ttt act tgt tta gcc tgg agt taa attcccactc	254
	Phe Phe Leu Leu Phe Thr Cys Leu Ala Trp Ser *	
20	45 50	
	cttgtgagca cttctaattt gaaaatccac tttcttcaat attttcgaaa tttaaaactg	314
	atggatgacg tgacaaaact tccacgagtt aagaattctc cacctctgat ctcacgcgag	374
	cagggcacaa tccaaggcat gtgaattgac ttccagggtt atgtgacata taaatgaatt	434
25	ctgtctctag atttggatcc cattctocta aatatctcac catgcatgtg cagatattct	494
	aaagtctaaa aatatctgat attgcaaact tttctgggtca aaacattttg gatgagccat	554
	ttaacagcca aggtatttga gacagagggt tcaacagcat tcctggagga gacacaaagg	614
	acagatgagt cacatgaagg atgggaggag ggaagggtggc tgttgatagg tatttttgaga	674
	cactctattt gagtcctaca caacactccc cctccccccc ctccccccaa accattttta	734
30	tgtctattga cctttcctct agtcatacag ggacattcac agttacctac aaagaaccag	794
	aattgtaaca agtcaagagg aaacttattt ttgataatga ctcatgaag atgttttgaa	854
	aatttaaaaa taagctcttg taagcagaag tctgtgagaa aagcaagaag gaattgtttg	914
	tttattaaat aaataaaaagg cnnannnnnaa aaaaaaaaaa aaaaangcgg ccgc	968
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FIGURE 32

5	tctagcgaac cccttoggca gacagcatcc ctcccaaggc tactcagggt ttaaaccctg	60
	cttctgaagt gacatgtcct gcaaagaaag tccccacgtg ggtgtttcca ccaccactgt	120
	cagctctgta gctgtgcaag ctggggactc caagatcgtg atagccgttg tcaagtgtgg	180
	caaatgggtg cggctccaac tggctgaggc acagcccaat ctccctagaaa ttgggagcag	240
	tcaag atg aaa cca gaa aac tgc ttc acg atc acg agc tcc ttc tgg cca	290
10	Met Lys Pro Glu Asn Cys Phe Thr Ile Thr Ser Ser Phe Trp Pro	
	1 5 10 15	
	agc tta agg cct tgg aag atc gtg tgt ggg gac tct tac agg aag cag	338
15	Ser Leu Arg Pro Trp Lys Ile Val Cys Gly Asp Ser Tyr Arg Lys Gln	
	20 25 30	
	aca gga cgg ctg aag caa aca agg agc aaa gtg agg tgt cga tgc cat	386
	Thr Gly Arg Leu Lys Gln Thr Arg Ser Lys Val Arg Cys Arg Cys His	
	35 40 45	
20	ggc cag act ctg ggc gaa gca tgg gcc acc ctg gtc ttc atg ctt gaa	434
	Gly Gln Thr Leu Gly Glu Ala Trp Ala Thr Leu Val Phe Met Leu Glu	
	50 55 60	
25	aga aga agg gag ctc ctc gga ctg aca tct gag ttt ttt caa agc gcc	482
	Arg Arg Arg Glu Leu Leu Gly Leu Thr Ser Glu Phe Phe Gln Ser Ala	
	65 70 75	
30	ttg gag ttt gct ata aaa ata gac caa gct gaa gat ttt ctg cag aat	530
	Leu Glu Phe Ala Ile Lys Ile Asp Gln Ala Glu Asp Phe Leu Gln Asn	
	80 85 90 95	
35	cct cac gag ttt gag agt gcc gaa gcc tta cag tca ctt ctt ctg ctt	578
	Pro His Glu Phe Glu Ser Ala Glu Ala Leu Gln Ser Leu Leu Leu Leu	
	100 105 110	
	cat gac cga cac gcc aaa gaa ctc tta gaa cga tct cta gtc ctt tta	626
	His Asp Arg His Ala Lys Glu Leu Leu Glu Arg Ser Leu Val Leu Leu	
	115 120 125	
40	aac aaa agc caa caa ctc act gac ttc ata gaa aaa ttc aag tgt gat	674
	Asn Lys Ser Gln Gln Leu Thr Asp Phe Ile Glu Lys Phe Lys Cys Asp	
	130 135 140	
45	gga tct cct gtg aat tct gag ctc atc cag gga gct cag agc agt tgt	722
	Gly Ser Pro Val Asn Ser Glu Leu Ile Gln Gly Ala Gln Ser Ser Cys	
	145 150 155	
50	ctg aag atc gac agc ctc ctt gaa ctt ctg caa gac agg aga agg cag	770
	Leu Lys Ile Asp Ser Leu Leu Glu Leu Leu Gln Asp Arg Arg Arg Gln	
	160 165 170 175	
55	ctg gac aag cac ttg cag caa cag agg cag gag ttg tct cag gtt ctg	818
	Leu Asp Lys His Leu Gln Gln Gln Arg Gln Glu Leu Ser Gln Val Leu	
	180 185 190	
	cag tta tgt ctg tgg gac caa caa gaa agc cag gtt tct tgt tgg ttt	866

FIGURE 32 (cont.)

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FIGURE 33

5	tctagcgaac	cccttcgcgc	aagatggcgc	cttcccagac	cgctccgcgc	catcttcaag	60
	atgcgcgaga	agaacgtgca	atctcgcgag	atcaggctcg	ctcgcgggca	gtctgctcgc	120
	agcctacct	tcctaggagt	tgaggagg	aaagctagat	tcgattaaga	gcaaaaaatt	180
	gttccagcag	cagagcagct	gtccaaggaa	gtatccaaag	gaactgcacc	tcagtaaact	240
	cctggcaagt	cttaggatat	gacaaagggc	acaggatgca	ttatgagaaa	ggaaggctaa	300
10	ggttttcaag	aacacagatt	tacatcaaac	ttgcgttctg	aattaatctt	tgagaatact	360
	ggactgtgag	ctagacattg	agtaagaggt	ttgttatatc	aagaatgtga	tctaaaaaaa	420
	aaacattcat	atcttcctcc	cacaagagga	tattttgaaa	ctgtgggtca	aagtcagact	480
	acaggagagc	cctcaaatat	gccaaatgtg	acagacagca	ggattttgaa	aatatagtgg	540
	gagtatgtga	agatgttcca	gtcaaagaga	cattgtttcc	aaaggaaaaga	aagtccagtc	600
15	gcctcacagg	aattgtgtat	tccttggtag	taatgcaa	ggaccacata	tggttttctt	660
	ctttaaagag	aataccta	tttagctaca	gagtaaaatg	ctgatgatac	aaaccgtgac	720
	aagtggagg	acaagaaagt	aaatggactg	atggtgccat	tgtggactgg	gagggtaaaa	780
	gctgtacatt	tgtgaacaaa	aagatttctt	tgttatggtc	agccatgatt	ctaactgcta	840
	aatggaggca	gtaacaacat	gacctaaaga	gtaaacatcc	agagatggaa	tgttctcaat	900
20	gtctgaaaag	gagcagatat	ctggtgtatg	tgaatgtatg	ctagagattt	tttacaagcc	960
	tgtggtgaat	tagtaattgt	attttatttt	gaaagttaaa	caggtaatta	gaaaccccaa	1020
	aaaaaaaaa	aataaaaaa	aagcggcgc	c			1051
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FIGURE 34

5	tctagcgaac	cccttcgctg	aaaccacagt	tcacacggga	aacctggggt	aggtttttgt	60
	cctcagtgac	acagaggatg	tagtccacag	ctaggtagaa	atgtcagggt	cccaacacta	120
	ctccagctgt	gactttgatg	cttgggggat	ggggctgcag	gctattttct	ctgctttaac	180
	agttcataga	atttaacaga	ttaaggttag	tgtctttcat	gtggcctcac	tctggagtta	240
	tgagaacata	cacacggttt	acagcttttc	aatatncott	tccctggcca	tcaagtattt	300
10	tgaagtgtg	ccacctttta	acctttgcgc	tttatttttt	tttctttttt	taaagntgaa	360
	ggtgataatt	cttctatata	tgatgaaact	caatgtctac	tgaataaagt	gtaaccttag	420
	ctatncacgt	ttatntttta	aaaccacgct	atggagatat	taccccgagt	tctgtcnttt	480
	ngcaagattt	acagnacctt	ccnccccccc	cttttagcat	tnaataaaaa	natattgggg	540
	agcncnntna	aaaaaaaaaa	aatnaaaaaa	agcggc			576

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FIGURE 35

5	tctagcgaac cccttcgcgt gatctgatcc gagctgagac ttggggagct ctggctccgt	60
	gttggtgca gcattcccca tggcttctgc tgaggtgtcc tgtgactcga ctcttcagaa	120
	ctcaatgaag tagatgactt gactacaatg tggaaacatc atg aca gaa agt gtg	175
	Met Thr Glu Ser Val	
	1 5	
10	gtt tgt acc ggg gcc gtc agc act gta aag gaa gtc tgg gaa gaa aga	223
	Val Cys Thr Gly Ala Val Ser Thr Val Lys Glu Val Trp Glu Glu Arg	
	10 15 20	
15	ata aag aaa cat cat gaa gat gtg aaa cga gag aag gaa ttt cag caa	271
	Ile Lys Lys His His Glu Asp Val Lys Arg Glu Lys Glu Phe Gln Gln	
	25 30 35	
20	aag cta gtg cgg atc tgg gaa gac cga gtg agt tta act aag ctg aaa	319
	Lys Leu Val Arg Ile Trp Glu Asp Arg Val Ser Leu Thr Lys Leu Lys	
	40 45 50	
25	gag aag gtg acc agg gaa gat gga aga atc att cta agg ata gag aaa	367
	Glu Lys Val Thr Arg Glu Asp Gly Arg Ile Ile Leu Arg Ile Glu Lys	
	55 60 65	
30	gag gaa tgg aag act ctc cct tct tcc tta ctg aaa ctg aat cag cta	415
	Glu Glu Trp Lys Thr Leu Pro Ser Ser Leu Leu Lys Leu Asn Gln Leu	
	70 75 80 85	
35	cag gag tgg caa ctt cat agg acc gga ttg ttg aaa att cct gaa ttc	463
	Gln Glu Trp Gln Leu His Arg Thr Gly Leu Leu Lys Ile Pro Glu Phe	
	90 95 100	
40	att gga aga ttc cag cat ctc att ggt cta gac tta tct cgg aac aca	511
	Ile Gly Arg Phe Gln His Leu Ile Gly Leu Asp Leu Ser Arg Asn Thr	
	105 110 115	
45	att tca gag atc ccc ccg agg cat tgg act gnt cac tta gac ttc aag	559
	Ile Ser Glu Ile Pro Pro Arg His Trp Thr Xaa His Leu Asp Phe Lys	
	120 125 130	
50	gaa ctg att ctt agc tac aca aaa tca a	587
	Glu Leu Ile Leu Ser Tyr Thr Lys Ser	
	135 140	

FIGURE 36

5	tctagcgaac	cccttcgggt	ctgttggtta	cacagctgca	gagccatggc	tgaccgttca	60
	ctgtcagggg	cacatgttac	actaagcttc	atgacagtga	tgtaataatg	ttacacattt	120
	gtcttgtagt	tatgtattga	agtttctgtc	ctgttttgtg	taaaaatgta	tccactcttg	180
	tatatattta	gacttgaaac	taccacacaa	atattggaac	ggtttgcttt	atgaagttaa	240
	aagtatcctt	ccgaatggaa	ctaacttgct	ttgtgctcag	acataatact	tgctgatgta	300
10	ttttgcaata	tactatctta	aattaaatct	ggtcactttg	ttgccttttt	aaaaagtgtg	360
	gtatttcaag	tagagttatt	ttcctgaaat	atatttgcaa	actcaagctg	ctttataatc	420
	aaggaatatt	tttattgatt	gaagaaaatg	actgctgcaa	ttcaaaaagt	aacttatttt	480
	attatataga	tgatttctta	aaagctatatt	ataccatgat	acaaaatcat	gtagtgatcc	540
	tgggagtctg	tagttcttcc	tgtttaataac	attcaacact	gtatgctaga	ggcagcaatg	600
15	ccaacactga	agttattttg	ggtgaaaacc	gtcgttctgn	cctgttttagc	tggggattat	660
	taaatccata	taatgtatgt	gcttatgtat	gctacatgtg	caagttaggt	gtttcctttg	720
	tgttctgctt	attaaatgtc	attcagattc	acttcctgaa	ttctaataaa	gaggggaagct	780
	attggaaaaa	ataaaaaaaa	aaaaaaaaaa	gcggccgcc			819

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FIGURE 37

[illegible]

FIGURE 38

5	tctagcgaac	cccttcgtag	aactaggagc	cagtgttgac	cacggtcggt	ggctggatac	60
	cccactgcat	gotgcagcaa	ggcagtcag	tgtggaggtc	atcaatctgc	toactgagta	120
	tggggctaac	ctgaaactca	gaaactcgca	gggcaaaagt	gctcttgagc	tcgctgctcc	180
	caaaagtagt	gtggagcagg	cactcctgct	ccatgaaggt	ccacctgctc	tttctcagct	240
	ctgccgcttg	tgtgtccgga	agtgcttggg	cgcac atg	tca tca agc cat cta		294
10				Met	Ser Ser Ser Ser	His Leu	
				1		5	
	cgc act agg tct gcc aga acc cct gga aaa att cct ctt ata cca ata						342
	Arg Thr Arg Ser Ala Arg Thr Pro Gly Lys Ile Pro Leu Ile Pro Ile						
15		10		15		20	
	gtt gga aac atg ttg cct gct gta gga cac tta ata tac aca ttc agt						390
	Val Gly Asn Met Leu Pro Ala Val Gly His Leu Ile Tyr Thr Phe Ser						
		25		30		35	
20	ggc tta acc cac tat cct aaa aat ctg ctt acc taa ttagaataaa						436
	Gly Leu Thr His Tyr Pro Lys Asn Leu Leu Thr *						
		40		45			
25	gccttcataa atccaaatac ttgogttgaa caaactcctg gttagggttaa tggntgccaa						496
	gagataacca gaaacctttc aagtttttaa ctcttggttaa tttaaaatca aactgaaata						556
	gatggaaaat aataatctat ttttggataa ttcaaggacc cttcagtatc tggggctggg						616
	gtccgcattt tgnatactgg atagacacac acacaggtag gatanggtaa atnaactact						676
	taaagaatgg cctgggattt aagtcctcca gatatttttt aggtngnggt ttctctaaaat						736
30	aaaattctgg agtgccaaaa aaaaaaaaaa aaaaaaaaaa cgggcc						782
35							
40							
45							
50							
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FIGURE 39

5	gtctagcgaa ccccttcggg aaacttcaac aaaggtacca gcaactacag cgccttgccc	60
	accagattt cttcagccaa aagtctcaga ctgagaaacg gttctcggag aagcattcga	120
	ccctgggtgaa tgatgcctac aagactcttc agggcccccgt gagcagagga ctatatcttc	180
	taaagctcca aggaatagaa attcctgaag ggacagatta tagaacagac agtcagttcc	240
	ttgtggaaat c atg gaa atc aat gaa aaa ctc gca gac gcc aaa agt gag	290
10	Met Glu Ile Asn Glu Lys Leu Ala Asp Ala Lys Ser Glu	
	1 5 10	
	gca gcc atg gaa gag gta gaa gcc act gtc aga gct aaa cag aaa gaa	338
	Ala Ala Met Glu Glu Val Glu Ala Thr Val Arg Ala Lys Gln Lys Glu	
15	15 20 25	
	ttt acg gac aat ata aac aga gct ttt gaa caa ggt gat ttt gaa aaa	386
	Phe Thr Asp Asn Ile Asn Arg Ala Phe Glu Gln Gly Asp Phe Glu Lys	
	30 35 40 45	
20	gcc aag gaa ctt ctt aca aaa atg aga tac ttt tca aac ata gaa gaa	434
	Ala Lys Glu Leu Leu Thr Lys Met Arg Tyr Phe Ser Asn Ile Glu Glu	
	50 55 60	
25	aag atc aag tta agc aag aac cct ctc tag ttgctaactt aaaggtttaa	484
	Lys Ile Lys Leu Ser Lys Asn Pro Leu *	
	65 70	
	aaataaaactt tgtatttctt cannnnnnan nnnnannntn nnnnagcggc cgcc	538
30		
35		
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FIGURE 40

5	tctagcgaac	cccttcgoga	aggggttcgc	ttcttaccct	gtggagaaag	gggcaggagg	60
	aacctcctgt	gttaggagga	agctggagct	taccactgtg	agaggacaga	tgtggactga	120
	gaattttctt	agtgtcagt	ggcacttccc	aaggactccc	ctccccttgt	gctctgtgcg	180
	gttttttagga	cagctaagat	gactgccacc	tggtgtggca	ggcccgattt	gtcttgttct	240
	ccccttactg	taccccgata	taatctctgt	tgatcaacag	gactacccca	agaatccaca	300
10	tgttctcccc	cgtaaccagg	cagctgtctg	gttcatgcct	tcttcccttc	aaacccaacc	360
	cagcgccctt	gttagtgaag	aggtgggtcca	tggaactgatg	acaagttatt	agcactggat	420
	gctgtttcca	tagtgacaag	cctatacctc	ttcccaccct	ttagtgcgca	gtgggctgct	480
	gcttcagtat	cctcccagct	cagtttttatt	agatcaaagc	tgcccttggg	caccatgttg	540
	gccacctcaa	tcaccagcca	aaatgggtgc	tttgtccacc	agaggtcaag	ccatctttct	600
15	ggcgtgtag	ttcccagctc	cttctagggg	acaggaagtt	gatattgcca	tgggggaggt	660
	ggcggggtgt	ggcgcgtcacc	tcaatagttt	tactgtaaaa	gggaaatttg	aacaagaaca	720
	acaacaaaaa	aaaaaaaaaa	acaaagaaaa	aaataaaaaa	ctttaaaagt	tgaaaaaaaa	780
	aaaaaaaaaa	aaaaaaagcg	gccgc				805

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FIGURE 41

5	tctagcgaac cccttcgctg ggaccgcgaa ctaccaactg ccgcctggat cctaggtgag	60
	ctgtggggctc tgacagcgct gtggctaac atg gca ccc aaa aag aag act ctc	113
	Met Ala Pro Lys Lys Lys Thr Leu	
	1 5	
10	aag aag aac aaa ccc gag atc aat gag atg acc atc atc gtg gaa gac	161
	Lys Lys Asn Lys Pro Glu Ile Asn Glu Met Thr Ile Ile Val Glu Asp	
	10 15 20	
15	agc ccc cta aac aag ctg aat gct cta aat ggg ctc ctg ggg gga gaa	209
	Ser Pro Leu Asn Lys Leu Asn Ala Leu Asn Gly Leu Leu Gly Gly Glu	
	25 30 35 40	
20	aac agc ctt agc tgt gtt tct ttc gaa cta aca gac act tct tat ggt	257
	Asn Ser Leu Ser Cys Val Ser Phe Glu Leu Thr Asp Thr Ser Tyr Gly	
	45 50 55	
25	ccc aac ctc ctg gaa ggt tta agt aaa atg cgt caa gag agc ttt cta	305
	Pro Asn Leu Leu Glu Gly Leu Ser Lys Met Arg Gln Glu Ser Phe Leu	
	60 65 70	
30	tgt gac ttg gtc atc ggt cca aaa cca agt cct ttg atg tcc ata agt	353
	Cys Asp Leu Val Ile Gly Pro Lys Pro Ser Pro Leu Met Ser Ile Ser	
	75 80 85	
35	caa gtg atg gct tcc tgc agc gag tct tct ata ata tcc tta aaa cga	401
	Gln Val Met Ala Ser Cys Ser Glu Ser Ser Ile Ile Ser Leu Lys Arg	
	90 95 100	
40	tcc atc gac aaa aag ggt aga cct caa tga tctcgncct ttagggctac	451
	Ser Ile Asp Lys Lys Gly Arg Pro Gln *	
	105 110	
45	caccgtgata gcatatgcat acacnggaaa gctgcccttt ctttatacac aataaggaag	511
	catcatttct gctgctgtgt acctccagat ccacactcct gtgaagatgt gcagcgactt	571
50	tctgatccga gagatcagtg ttgagaactg catgtatggt gttacatgg ctgaaacata	631
	ctgcttgaaa aatgcgaaa caacggcca gaaatttatc cgggataact tcattgaatt	691
	tgccgactcc gaacaattta tgaagctgac gtttgaacag attaatgagc ttctcataga	751
	tgatgacttg cagttgcctt ctgagctggt agcattccag attgcaatga aatggataga	811
	attcaaccaa aagagagtga agcacgctgc ggatctttta agcaatatc gctttggtac	871
55	catctctgca caagacctgg tcaattacgt tcaaaccgta ccgagaatga tgcaagacgc	931
	tgattgtcat aaactgcttg tggatgctat gaactaccac ttactacctt atcatcaaaa	991
	cacgttgcaa tctaggcgga caagaattag aggcggctgc cgggttctga tcaatgctcg	1051
	gggacgacct ggccgtgact agaagtcctt tagtagagac gtttatatag agacctgaa	1111
	aatggatgga gcaagcttac agaaatgcca gccaaagagt tcaatcagtg tgtggctgtg	1171
	atggatggat tcttttatgt agcaggtggt gaggaccaga atgatgcgag aaaccaagcc	1231
	aagcatgcag tcagcaattt ctgcaggtac cgatccccgc ttcaacacgt ggatccacct	1291
	gggcagcatg aaccagaagc gcacgcactt cagcctgagc gtgttcaacg ggctcctgta	1351
	cgccggtggn gggcnccagt gnganggata tctgcagaat tcggctagcc gaattc	1407

FIGURE 42

5	tctagcgaac cccttcggac actgccagca tagacagcag cccctgctac tgtcccacca	60
	ctgtaccccca gagccccgac tagcagt atg ccg gga gcg cca ggg cct ggg cct	114
	Met Pro Gly Ala Pro Gly Pro Gly Pro	
	1 5	
10	gag gtg gct gca gcc ttt gag gaa cgg ttg agt cag gca cta cag gaa	162
	Glu Val Ala Ala Ala Phe Glu Glu Arg Leu Ser Gln Ala Leu Gln Glu	
	10 15 20 25	
15	ctg cag gca gtg gct gaa gca ggc cgg tca gcg gtg acc cag gca gct	210
	Leu Gln Ala Val Ala Glu Ala Gly Arg Ser Ala Val Thr Gln Ala Ala	
	30 35 40	
20	gat gca gcc cta gcc act gta gag cca gtg gct cag gca tct gaa gag	258
	Asp Ala Ala Leu Ala Thr Val Glu Pro Val Ala Gln Ala Ser Glu Glu	
	45 50 55	
25	ctt cgg gcc gag aca gca gcc ctg agc cgg cgg ctg gat gcc ctg acc	306
	Leu Arg Ala Glu Thr Ala Ala Leu Ser Arg Arg Leu Asp Ala Leu Thr	
	60 65 70	
30	agg cag gtg gag gtg ctg agc cta cgg ctg ggt gtt cca ctc gtg ccg	354
	Arg Gln Val Glu Val Leu Ser Leu Arg Leu Gly Val Pro Leu Val Pro	
	75 80 85	
35	gac ctg gag tcc gag cta gag ccc agc gag ctg ttg ctg gct gct gcc	402
	Asp Leu Glu Ser Glu Leu Glu Pro Ser Glu Leu Leu Leu Ala Ala Ala	
	90 95 100 105	
40	gac cct gag gcc ctc ttc cag gca agc tga gcatgctggg acccccgtgg	452
	Asp Pro Glu Ala Leu Phe Gln Ala Ser *	
	110	
45	ccacccgcct gccttttagca cccgccgcag ctctttctgcg ggccctctct gaagcagcag	512
	tctcatggag cccgatccag cagagcccc ctctgccaca gtggaagcag ctaatggaac	572
	agagcagact ctggacaaag tgaacaaagg cccagagggg cggagcccc tgagtgcaga	632
	ggagctgatg gccattgagg acgaaggaat cctggacaag atgctggacc aggctacgaa	692
	ctttgaagag cggaagctca tccgggctgc gctccgtgag ctccgacaaa gaaagagaga	752
	ccagagggac aaggaacgag aacggcggct acgagaggca cgggcccggc caggcgagag	812
	ccgaagcaat atggctacta cagagaccac caccaggcac aagccagagg gcggctgatg	872
	gctcggcggt cagcacagtt accaaaactg agcgggtcgt ccaactccaat gacggcacgc	932
	agactgcgag caccaccaca gtggagtcga gtttcgtgag gcgctcggag aatggcagca	992
	gcaagcaagc agcagcacca cggtcctaac caagaccttt tctcttctct ctctctctct	1052
	caaaaaaatg ggcagtatct tcgaccgaga ggaccaaacc agctcacggt ctggcagcct	1112
	ggcggccctc gaaaaacgcc aggcagagaa gaagaaagag ctcatgaagg cacagagtct	1172
	gcccgaagac taagcgtccc aagcacgcaa ggccatgatt gagaaaactag agaaggaagg	1232
	ctcttcgggc agtcctggca caccocgtac agcggtagag cgttctacca gcttcggagt	1292
	ccccaacgcc aacagcatca agcagatggt gctggactgg tgccgagcca agaccocgtg	1352
	ctacgagcac gtggacatcc agaacttctc tccagctgga gtgatgggat ggctttctgt	1412
	gccctggtgc acaatttctt ccttgaggct tttgactatg gacagcttag cccacaaaac	1472
	cggcgccaga actttgaaat ggccttctca tctgctgaga cccatgcgga ctgcccgcag	1532
	ctcctggata cagaggacat ggtgcggctt cgagagcctg actggaagtg cgtgtacacg	1592
	tacatccagg agttctaccg ctgtctggtc cagaaggggc tggtaaaaac caaaaagtcc	1652

taacccctgc ttggggcccc acggatgctg gtggactgtg taccottggt ggaggtggag 1712
gacatgatga tcatgggcaa aaagccagac cctaagtgcg tottcaccta cgtgcaatcg 1772
FIGURE 42 (cont.)

5 ctgtacaacc acctgcgcg ccatgagctg cgctgcgcg gcaagaatgt ctagccactg 1832
ctcacaccgc ctgcgctgca ggctgctgtc ccacgcccc aacaccggnc cctncagtgn 1892
gcctgccact gntgcccgtg tgcgaaaca cctntccct tgccacacgc agngntttga 1952
taaattattt gntttnaaca aaaaaaaaaa aaaaaaaaaa aaaagcggcc gc 2004

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FIGURE 43

5	tctagcgaac cccttcgctc cagggcggtt gccctcctgct gacttgctct tcaccattag	60
	acaagcctga cgtcaagacc cca atg gct aac gaa gct aac cct tgc cca tgt	113
	Met Ala Asn Glu Ala Asn Pro Cys Pro Cys	
	1 5 10	
10	gac att ggt cac agg cta gac tat ggt ggc atg ggc cag gaa gtt cag	161
	Asp Ile Gly His Arg Leu Asp Tyr Gly Gly Met Gly Gln Glu Val Gln	
	15 20 25	
15	gtt gag cac atc aag gca tat gtc acc cgg tcc cct gtg gat gca ggc	209
	Val Glu His Ile Lys Ala Tyr Val Thr Arg Ser Pro Val Asp Ala Gly	
	30 35 40	
20	aaa gct gtg att gtt gtc cag gat ata ttt ggc tgg cag ctg tcc aac	257
	Lys Ala Val Ile Val Val Gln Asp Ile Phe Gly Trp Gln Leu Ser Asn	
	45 50 55	
25	acc agg tat atg gct gac atg att gct gga aat gga tac aca act att	305
	Thr Arg Tyr Met Ala Asp Met Ile Ala Gly Asn Gly Tyr Thr Thr Ile	
	60 65 70	
30	gcc cag act tct ttg tgg gtc aag agc cat ggg acc cgg ctg gtg att	353
	Ala Gln Thr Ser Leu Trp Val Lys Ser His Gly Thr Arg Leu Val Ile	
	75 80 85 90	
35	ggg cca cct tcc ctg agt ggt tga aatcaagaaa tgccagaaaa atcaaccgag	407
	Gly Pro Pro Ser Leu Ser Gly *	
	95	
40	aggttgatgc tgtcttgagg tatctgaaac aacagtgtca tgcccagaag attggcattg	467
	tggtgttctg ctgggggggt attgtggtgc accacgtgat gacgacatat ccagaagtca	527
	gagcgggggt gtctgtctat ggtatcatca gagattctga agatgtttat aatttgaaga	587
	acccaacggt gtttatcttt gcagaaaatg atgctgtgat tccacttgag caggtttcta	647
	tactgatcca gaagcttaaa gaacactgca tagttaatta ccaagttaag acattttctg	707
	ggcaaaactca tggctttgtg catcggaaga gagaagactg ctcccctgca gacaaaccct	767
	acattgagga agcgaggagg aatctcatcg aatggctgaa caagtatatt taacagcact	827
	caagcacaaa ttttgaataa ttaaattgac ccgaataatt aaattgaccc gaat	881

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Case: SCIOS.017A
Applicant: Stanton et al.
For: SECRETED FACTORS
Sheet 57 of 59 drawings

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620 Newport Center Drive
Sixteenth Floor
Newport Beach, California 92660
(949) 760-0404

FIGURE 44

Regulated expression of Full-length novel clones:

[illegible]

FIGURE 44 (CONT.)

Seq ID	CloneID	Kidney		Hyp 10w	Heart						Spt				
		PKD	Na + Ang2		2w	4w	8w	12w	16w	2w	4w	8w	12w	16w	
30	P00249_F09			—	▲	▲	▲	▲	▲	—	▲	—	▲	▲	
31	P00258_A10			—	▲	▲	▲	▲	▲	—	—	—	—	—	
32	P00262_C10			▲	—	▼	—	—	—	—	—	—	—	—	
33	P00263_G06			▲	—	—	—	—	—	—	—	—	—	—	
34	P00267_F08	—	—	▼	—	▲	—	▲	—	—	—	—	—	—	
35	P00269_H08			▲	—	▼	—	▼	▼	—	—	—	—	—	
36	P00312_C04				—	—	▼	—	—	—	—	▼	—	—	
37	P00324_H02				—	▼	▼	▼	—	—	▼	▼	▼	▼	
38	P00628_H02	▲	—	—	—	—	▲	▼	▼	—	—	—	—	—	
39	P00629_C08			—	—	▼	—	—	▼	—	—	—	—	—	
40	P00634_G11														
41	P00641_G11	—	—	▲	—	—	—	—	—	—	—	—	—	—	
42	P00648_E12														
43	P00697_C03	▼	—	—	—	—	—	▼	▼	—	—	—	—	—	